

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; SS.  
 OS Homo sapiens.  
 XX  
 XX W0200062734-A2  
 XX  
 XX 26-OCT-2000.  
 XX  
 XX 24 MAP-2000 2000W07080020  
 XX  
 XX 06-APP-1999 980S-0127954  
 XX  
 XX (UVEC-) UNIV EAST CAROLINA.  
 XX (NYCE/) NYCE J W.  
 XX  
 XX NYCE JW;  
 XX  
 XX WPI: 2000-6/06/04/66  
 XX  
 XX Low adenosine (A) content antisense oligonucleotides which do not  
 PT trigger adenosine receptors during metabolism, useful e.g. for treating  
 PT cancers and respiratory obstructions -  
 XX  
 XX  
 PS Claim 14, page 241: 1592pp; English.  
 XX  
 XX The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (1) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a thioester or alternative base  
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antitasthma, hypertensive and cytostatic activities.  
 CC The antisense oligonucleotides and (1) can be used to down-regulate the  
 CC expression and/or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and nonnervous system  
 CC receptors, CNS and peripheral neurons and nonnervous system peptide  
 CC transmitters, growth factors, vasorelaxant proteins, and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies),  
 CC and/or tumor and hyperinflation which are associated with a disease;  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impaired respiratory, respiratory distress syndrome  
 CC (ARDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAT8433 to AAT21513 represent human P-12a, P-12b,  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention.  
 XX  
 XX Sequence 28 BP; 0 A; 10 C; 9 G; 9 T; 0 other;  
 SO  
 Query Match: 0.94; Score 28; 19 bits; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1504 aagagcagagcagagcagagcagagc 1531  
 Db 28 AAGAGCGCAGGCGCGACGACGCGACG 1  
 RESULT 16  
 AAA33977/c  
 ID AAA33977 standard; DNA: 28 BP.  
 XX

AC AAA33977;  
 XX  
 XX 28-JUL-2000 (first entry)  
 DE  
 XX Low adenosine antisense oligonucleotide SEQ ID NO:1666.  
 XX  
 XX Homo sapiens.  
 XX  
 XX W0200009525-A2.  
 XX  
 XX 24 FEB-2000.  
 XX  
 XX 03 A03-1999 99W070817712.  
 XX  
 XX 03 A03-1998 980S-0095212.  
 XX  
 XX (UVEC ) UNIV EAST CAROLINA.  
 XX  
 XX NYCE JW;  
 XX  
 XX WPI: 2000-2004/1718.  
 XX  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers -  
 XX  
 XX  
 PS Claim 18, page 471, 1344pp; English.  
 XX  
 XX The present invention describes a new composition comprising an  
 CC antisense oligonucleotide (OB) with low adenosine (up to 15%), which  
 CC targets certain aids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The OB can have antiinflammatory, antiallergic,  
 CC antitasthma, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects affect the lungs of a subject. They can be used for treating  
 CC e.g. bronchial conditions, pulmonary vasoconstriction, allergy,  
 CC asthma, impaired respiratory, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancer, such as lung cancers, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of  
 CC the OBs reduces side effects. The A containing OBs break down with the  
 CC release of a cytochrome which in turn causes the receptors causing  
 CC bronchoconstriction and inflammation. AAA42413 to AAA56412 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 185, and then the last  
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
 CC (AAA42413 to AAA33992) are specifically aligned CNS from the present  
 CC invention. H.B. sequences given in the disclosure of the present  
 CC invention do not match up with their corresponding SEQ ID NO. sequences  
 CC given in the sequence listing.  
 XX  
 XX Sequence 28 BP; 0 A; 11 C; 10 G; 7 T; 0 other;  
 SO  
 Query Match: 0.94; Score 28; 19 bits; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 846 ccccaagagcagagcagagcagagcagagc 873  
 Db 28 AAGAGCGCAGGCGCGACGACGCGACG 1







XX (CETU ) CETUS CORP.  
PA  
XX  
XX  
PI Baer BW, Groves ES, Houston LT, Levenson CH.  
XX  
XX WP1: 1991-132642/18.  
DR  
XX Conjugates for e.g. AIDS or cancer therapy - has one or more anti-  
PI sense oligonucleotide(s) bound to ligand-binding mol. recognising  
PT cell surface molecule  
XX  
XX  
PS Claim 18: page 33; 50pp; English.  
CC  
XX The anti-sense oligonucleotide is complementary to the mRNA. It is  
CC conjugated to a cell surface ligand-binding molecule (e.g. growth  
CC factor (GF), antibody to GF, antibody to cell surface receptor or  
CC antibody capable of recognising complex comprising GF and GF  
CC receptor). Conjugation is pref. via a disulphide bond.  
CC The Ab-oligonucleotide conjugate is used to prevent or suppress TNF  
CC induced diseases in animals.  
CC See also AAQ11585-Q11593 and AAQ11595-Q11600.  
CC  
XX  
SU Sequence 29 BP; 3 A; 8 C; 6 G; 12 T; 0 Other;  
  
Query Match 0.88; Score 29; DB 12; Length 29;  
Best Local Similarity: 100.0%; Prod No. n.00;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 785 gaagagacacacatgagccttgaagatgatg atg  
- |||||  
DB 29 GAAGTACACCAATGACGACTGAAACATAT 1  
  
RESULT 7  
AAQ40907%  
ID AAQ40907 standard; DNA; 29 BP  
XX  
XX AAQ40907:  
AC  
XX  
XX 07-SEP-1993 (first entry)  
DI  
XX  
XX  
DE TNF oligonucleotide.  
XX  
XX Doublet; triplet; helix; duplex; triplex; major groove;  
KW TNF; sepsis; tumour necrosis factor; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX W09309813-A.  
PN  
XX  
XX 27-MAY-1993.  
PD  
XX  
XX 10-NOV-1992; 92W1-GP02073.  
PE  
XX  
XX 12-NOV-1991; 91GR-0023947.  
PR  
XX  
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
PA  
XX  
XX Epenetos AA.  
PI  
XX  
XX WP1: 1993-182253/22.  
DR  
XX  
XX  
PT (ppl. comprising anti-sense oligo nucleotide and radioactive  
PI moiety - for treating viral infection; sepsis, leukaemia and  
PT tumours  
XX  
XX  
XX Disclosure: Page 6; 43pp; English.  
CC  
XX Examples of antisense oligonucleotides that can be used for  
CC preventing or suppressing TNF induced diseases; for example sepsis,  
CC are those complementary to TNF DNA or RNA. For example, oligo  
CC nucleotides complementary to the following can be used: sequences

Query Match	0.884	Score 297	DB 141	Length 297
Post Local Similarity	100.00%	Prod. No. 0.097		
Matches	29	Mismatches	0	Indels
			0	Gaps
			0	
<p>around the 5' end of the TNF messenger RNA sequences at the beginning of and within the mRNA region coding for the 118 amino acid domain of the TNF protein; and sequences within the coding region of the 17 kb wnt. Examples of the specific oligonucleotide sequences complementary to the above mRNA regions are given in AAC40905-10.</p> <p>Sequence 29 BP: 3 A, 8 G, 6 C, 12 T, 0 other.</p>				
<p>Query Match</p> <p>Post Local Similarity 100.00% Prod. No. 0.097</p> <p>Matches 29 Mismatches 0 Indels 0 Gaps 0</p>				
<p>0.884 Score 297 DB 141 Length 297</p> <p>Prod. No. 0.097</p> <p>Mismatches 0 Indels 0 Gaps 0</p>				
<p>around the 5' end of the TNF messenger RNA sequences at the beginning of and within the mRNA region coding for the 118 amino acid domain of the TNF protein; and sequences within the coding region of the 17 kb wnt. Examples of the specific oligonucleotide sequences complementary to the above mRNA regions are given in AAC40905-10.</p> <p>Sequence 29 BP: 3 A, 8 G, 6 C, 12 T, 0 other.</p>				



CC The anti-sense oligonucleotide is complementary to TNF mRNA. It is  
 CC conjugated to a cell surface ligand-binding molecule (e.g. growth  
 CC factor (GF), antibody to GF, antibody to cell surface receptor or  
 CC antibody capable of recognising complex comprising GF and GF  
 CC receptor). Conjugation is pref. via a disulphide bond.  
 CC The Ab-oligonucleotide conjugate is used to prevent or suppress TNF  
 CC induced diseases in animals.  
 CC See also AA011585-Q11594 and AA011596-Q11600.  
 XX  
 SU Sequence 30 BP; 13 A; 3 C; 12 G; 2 T; 0 other;

Query Match 0.8%; Score 30; DB 12; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.037;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 886 ttgttctcagacctcttctctctctgac 915  
 |||  
 DB 30 ttgttctcagacctcttctctctctgac 1

## RESULT 2

AA040908/c  
 ID AA040908 standard; DNA: 30 BP.

AC AA040908;

DI 07-SEP-1993 (first entry)

DE TNF oligonucleotide.

XX Double; triple; helix; duplex; triplex; major groove;

KW TNF; sepsis; tumour necrosis factor; ss.

OS Synthetic.

PN W09309413-A.

XX 27-MAY-1993.

XX 10-NOV-1992; 92MO-GB02073.

XX 12-NOV-1991; 91GR-0021447

XX (IMCP) IMPERIAL CANCER RES TECHNOLOGY.

XX Epenetos AA;

DP WPI: 1993-182253/22.

PT Cpd. comprising anti-sense oligonucleotide and radioactive  
 PT moiety for treating viral infection, sepsis, leukaemia and  
 PT tumours

XX Disclosure: Page 6; 43pp; English.

CC Examples of antisense oligonucleotides that can be used for  
 CC preventing or suppressing TNF-induced diseases, for example sepsis,  
 CC are those complementary to TNF DNA or RNA. For example, oligo-  
 CC nucleotides complementary to the following can be used: sequences  
 CC around the 5' end of the TNF messenger RNA; sequences at the  
 CC beginning of and within the mRNA region coding for the transmembrane  
 CC domain of the TNF protein; and sequences within the coding region of  
 CC the 17 kD mol. Examples of the specific oligonucleotide sequences  
 CC complementary to the above mRNA regions are given in AA040908-10.  
 XX  
 SU Sequence 30 BP; 13 A; 3 C; 12 G; 2 T; 0 other;

Query Match 0.8%; Score 30; DB 14; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.037;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 886 ttgttctcagacctcttctctctctgac 915  
 |||  
 DB 30 ttgttctcagacctcttctctctctgac 1

## RESULT 3

AA179710/c  
 ID AA179710 standard; DNA: 40 BP.

AC AA179710;

DI 30-DEC 1997 (first entry)

DE Tumour necrosis factor-alpha probe.

XX Vaccine: hrb gene; Gram-negative bacterium; non-toxic mutant;  
 KW pathogen; endotoxin; diagnosis; passive immunisation;  
 KW Haemophilus influenzae; tumour necrosis factor alpha; TNF; probe;  
 KW ss.

OS Synthetic.

PN W09719688-A1.

XX 05-JUN 1997.

XX 27-NOV 1996; 96MO-0518084.

XX 01-DEC-1995; 95OS-0565043.

XX (AMCY) AMERICAN CYANAMID CO.

XX (REGC) UNIV CALIFORNIA.

XX (IOWA) UNIV IOWA RES FOUND.

PI Apicella MA, Atumocham R, Gibson BW, Lee N, Sunshine MG;

XX WPI: 1997-310355/28.

XX New Gram-negative bacterial pathogen vaccines - comprising a hrb  
 XX mutant or an endotoxin isolated from an hrb mutant optionally  
 XX conjugated to a carrier protein.

XX Example 4; Page 63; 79pp; English.

CC This oligonucleotide is a probe for tumour necrosis factor (TNF)  
 CC alpha. It was used to measure TNF mRNA produced by SV40  
 CC transformed human respiratory epithelial cells and human primary  
 CC respiratory epithelial cells following endotoxin stimulation. The  
 CC amount of TNF mRNA detected is directly proportional to the toxicity  
 CC of the stimulating lipopolysaccharide. A reduced ability to  
 CC stimulate TNF is an indication of an hrb mutant (see AA025084) being  
 CC substantially reduced in toxicity due to the lack of one or more  
 CC secondary acyl chains in the lipid A portion of the endotoxin.  
 CC Mutants of the hrb gene (see also AA179708) or an endotoxin  
 CC produced by such a mutant, can be used in claimed vaccines against  
 CC Gram-negative bacterial pathogens.  
 XX  
 SU Sequence 30 BP; 6 A; 11 C; 7 G; 6 T; 0 other;

Query Match 0.8%; Score 30; DB 15; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.037;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 tctcttctctctctctctctctctctctct 223  
 |||  
 DB 30 tctcttctctctctctctctctctctctct 1

RESULT 4  
 AA179711  
 ID AA179711 standard; DNA: 30 BP.







VERSION A56965.1 GI:3712948  
 KEYWORDS  
 SOURCE unclassified  
 ORGANISM unclassified  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Stanley, M. A. and Scott, P. G.  
 TITLE TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED LESIONS USING INTERFERON- $\gamma$   
 JOURNAL PATENT: WO 9629091-A 24 SEP-1996  
 COMMENT  
 FEATURES  
 SOURCE  
 BASE COUNT 8 a 4 c 5 g 4 t  
 ORIGIN

Query Match 0.68; Score 21; DB 6; Length 21;  
 best local similarity 100.0%; Prod. No. 13;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 796 ataacctgaacatgaac 816  
 DB 1 ATTACATCTGAACATGAC 21

RESULT 43  
 A56996 21 bp DNA PAT 03 MAR-1998  
 LOCUS Sequence 54 from Patient W09629091.  
 DEFINITION A56996  
 ACCESSION A56996.1 GI:371279  
 VERSION  
 KEYWORDS  
 SOURCE unclassified  
 ORGANISM unclassified  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Stanley, M. A. and Scott, P. G.  
 TITLE TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED LESIONS USING INTERFERON- $\gamma$   
 JOURNAL PATENT: WO 9629091-A 24 SEP-1996  
 COMMENT  
 FEATURES  
 SOURCE  
 BASE COUNT 6 a 4 c 9 g 4 t  
 ORIGIN

Query Match 0.68; Score 21; DB 6; Length 21;  
 best local similarity 100.0%; Prod. No. 13;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2266 ggcctgaacatgaac 2256  
 DB 1 ggcctgaacatgaac 21

RESULT 44  
 A61445 21 bp DNA PAT 09 MAR-1998  
 LOCUS Sequence 14 from Patient W09710442.  
 DEFINITION A61445  
 ACCESSION A61445.1 GI:3719577  
 VERSION  
 KEYWORDS  
 SOURCE unclassified  
 ORGANISM unclassified  
 REFERENCE 1 (bases 1 to 21)  
 ORIGIN

TITLE CHIMERIC OLIGONUCLEOTIDES AND USES THEREOF IN THE IDENTIFICATION  
 OF ANTISENSE BINDING SITES  
 JOURNAL PATENT: WO 9710332-A 14 20-MAR-1997;  
 BRAX GENOMICS LTD (GB)  
 FEATURES  
 SOURCE  
 BASE COUNT 3 a 2 c 11 g 5 t  
 ORIGIN

Query Match 0.68; Score 21; DB 6; Length 21;  
 best local similarity 100.0%; Prod. No. 13;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2340 gctctgacacacacac 2360  
 DB 21 gctctgacacacacac 1

RESULT 45  
 A56997 21 bp DNA PAT 03 MAR-2000  
 LOCUS Sequence 54 from Patient W09629091.  
 DEFINITION A56997  
 ACCESSION A56997.1 GI:371279  
 VERSION  
 KEYWORDS  
 SOURCE unclassified  
 ORGANISM unclassified  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Stanley, M. A. and Scott, P. G.  
 TITLE TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED LESIONS USING INTERFERON- $\gamma$   
 JOURNAL PATENT: WO 9629091-A 24 SEP-1996  
 COMMENT  
 FEATURES  
 SOURCE  
 BASE COUNT 6 a 4 c 9 g 4 t  
 ORIGIN

Query Match 0.68; Score 21; DB 6; Length 21;  
 best local similarity 100.0%; Prod. No. 13;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 928 ataacctgaacatgaac 948  
 DB 21 ataacctgaacatgaac 1

Search completed: April 11, 2002, 06:42:16  
 Job time: 11848 sec

RESULT 38  
LOCUS 139742 22 bp DNA  
DEFINITION Sequence 15 from patent us 5616490  
ACCESSION 139742  
VERSION 139742.1 GI:2084222  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Sullivan, S.M. and Draper, K.G.  
TITLE Ribozymes targeted to TMR alpha. RNA  
JOURNAL Patent us 5616490-A 15 01-APR-1997  
FEATURES  
Source location/Qualifiers  
1..22  
/organism="unknown"

BASE COUNT 4 a 4 g 6 g 3 t  
ORIGIN

Query Match 0.68; Score 22; E-6; Length 22;  
Best Local Similarity 100.0%; Prod. No. 3.5;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 2309 tcaagacacacagctgctc 2330  
|||||  
Db 1 tcaagacacacagctgctc 22

RESULT 39  
LOCUS 139755 22 bp DNA  
DEFINITION Sequence 28 from patent US 5616490.  
ACCESSION 139755  
VERSION 139755.1 GI:2084235  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Sullivan, S.M. and Draper, K.G.  
TITLE Ribozymes targeted to INF-alpha. RNA  
JOURNAL Patent us 5616490-A 28 01-APR-1997  
FEATURES  
Source location/Qualifiers  
1..22  
/organism="unknown"

BASE COUNT 3 a 3 c 4 g 12 t  
ORIGIN

Query Match 0.68; Score 22; E-6; Length 22;  
Best Local Similarity 100.0%; Prod. No. 3.5;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3032 tctattatattgacctgta 3054  
|||||  
Db 1 tctattatattgacctgta 22

RESULT 40  
LOCUS 158777 22 bp DNA  
DEFINITION Sequence 24 from patent US 5652453.  
ACCESSION 158777  
VERSION 158777.1 GI:2478015  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Fiers, W., Tavernier, J., and Van Ostado, X.

TITLE DNAs encoding tumor necrosis factor alpha mutants  
JOURNAL  
FEATURES  
Source location/Qualifiers  
1..22  
/organism="unknown"

BASE COUNT 2 a 4 c 8 g 4 t  
ORIGIN

Query Match 0.68; Score 22; E-6; Length 22;  
Best Local Similarity 100.0%; Prod. No. 3.5;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 2231 gctctctctctctctctctct 2242  
|||||  
Db 1 gctctctctctctctctctct 22

RESULT 41  
LOCUS AS8251797 22 bp DNA  
DEFINITION Artificial reverse oligonucleotide primer sequence for tumor  
ACCESSION A1251797  
VERSION A1251797.2 GI:1994592  
KEYWORDS oligonucleotide primer.  
SOURCE Synthetic construct.  
ORGANISM Artificial sequence.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Maniatham, A.K., Sreek, V.K., and Nair, S.  
TITLE Reverse oligonucleotide primer (5' - 3') for tumor necrosis factor  
mRNA in human  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 22)  
AUTHORS Maniatham, A.K.  
TITLE Direct Substitution  
SUBMITTED (26 DEC 1999) Maniatham A.K., Department of Immunology,  
Sanjay Gandhi Postgraduate Institute of Medical Sciences, Varanasi  
India, Lucknow, UP 226 014, INDIA  
REVISED BY [3]  
3 (bases 1 to 22)  
REFERENCE 3 (bases 1 to 22)  
AUTHORS Maniatham, A.K.  
TITLE Direct Substitution  
SUBMITTED (18 DEC 2000) Maniatham A.K., Department of Immunology,  
Sanjay Gandhi Postgraduate Institute of Medical Sciences, Varanasi  
India, Lucknow, UP 226 014, INDIA  
COMMENT On Dec 19, 2000 this sequence version replaced q1-0682805.  
FEATURES  
Source location/Qualifiers  
1..22  
/organism="synthetic construct"  
/label="taxon:32630"

BASE COUNT 6 a 7 c 5 g 4 t  
ORIGIN

Query Match 0.68; Score 22; E-6; Length 22;  
Best Local Similarity 100.0%; Prod. No. 3.5;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 2459 gctctctctctctctctctct 2480  
|||||  
Db 22 gctctctctctctctctctct 1

RESULT 42  
LOCUS A56965 21 bp DNA  
DEFINITION Sequence 23 from patent W9629091.  
ACCESSION A56965

```

VERSION      AR100413.1  GI:12810761
KEYWORDS
SOURCE
ORGANISM     unknown
REFERENCE    1 (bases 1 to 22)
AUTHORS      Baker,B.P., Bennett,C.,Frank, Butler,M.M. and Shanahan,W.R., Jr.
TITLE        Antisense oligonucleotide modulation of tumor necrosis
              factor- $\alpha$  (TNF- $\alpha$ ) expression
JOURNAL      Patient : US 6080580 A 44 27 JUN 2000;
FEATURES     Location/Qualifiers
SOURCE       1..22
BASE COUNT   7 a 4 c 9 g 4 t
ORIGIN
Query Match 0.68; Score 22; DB 6; Length 22;
Host Local Similarity 100.0%; Prod. No. 3,57;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1602 gccctctgagctcagctgg 1623
DB 22 tctctctgagctcagctcagct 1

RESULT 44
LOCUS       AR149968      22 bp      DNA
DEFINITION  Sequence 44 from patient US 6228642.
ACCESSION  AR149968
VERSION    AR149968.1  GI:15114559
KEYWORDS
SOURCE     unknown;
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Baker,B.P., Bennett,C.,Frank, Butler,M.M. and Shanahan,W.R., Jr.
TITLE      Antisense oligonucleotide modulation of tumor necrosis
              factor- $\alpha$  (TNF- $\alpha$ ) expression
JOURNAL    Patient : US 6228642-A 44 08 MAY 2001;
FEATURES   Location/Qualifiers
SOURCE     1..22
BASE COUNT 7 a 4 c 9 g 4 t
ORIGIN
Query Match 0.68; Score 22; DB 6; Length 22;
Host Local Similarity 100.0%; Prod. No. 3,57;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1602 tctctctgagctcagctcagct 1624
DB 22 tctctctgagctcagctcagct 1

RESULT 45
LOCUS       112255      22 bp      DNA
DEFINITION  Sequence 24 from patient US 5422104.
ACCESSION  112255
VERSION    112255.1  GI:910278
KEYWORDS
SOURCE     unknown;
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Fiore,W., Tavernier,J. and Van Ostade,X.
TITLE      TNF mutants
JOURNAL    Patient : US 5422104 A 24 06 JUN 1995;
FEATURES   Location/Qualifiers
SOURCE     1..22

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```

BASE COUNT   2 a 8 c 8 g 4 t
ORIGIN
Query Match 0.68; Score 22; DB 6; Length 22;
Host Local Similarity 100.0%; Prod. No. 3,57;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2221 gccctctgagctcagctcagct 2242
DB 1 gccctctgagctcagctcagct 22

RESULT 46
LOCUS       117246      22 bp      DNA
DEFINITION  Sequence 14 from patient US 5486463.
ACCESSION  117246
VERSION    117246.1  GI:1252154
KEYWORDS
SOURCE     unknown;
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Lesslauer,W., Loischer,H. and Stuber,D.
TITLE      TNF mutants
JOURNAL    Patient : US 5486463-A 14 24 JAN 1996;
FEATURES   Location/Qualifiers
SOURCE     1..22
BASE COUNT 2 a 8 c 8 g 4 t
ORIGIN
Query Match 0.68; Score 22; DB 6; Length 22;
Host Local Similarity 100.0%; Prod. No. 3,57;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2221 gccctctgagctcagctcagct 2242
DB 1 gccctctgagctcagctcagct 22

RESULT 47
LOCUS       144465      22 bp      DNA
DEFINITION  Sequence 6 from patient US 5597899.
ACCESSION  144465
VERSION    144465.1  GI:1825256
KEYWORDS
SOURCE     unknown;
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Hammer,D., Lesslauer,W., Loischer,H. and Stuber,D.
TITLE      Tumor necrosis factor mutants
JOURNAL    Patient : US 5597899 A 6 28 JAN 1997;
FEATURES   Location/Qualifiers
SOURCE     1..22
BASE COUNT 3 a 4 c 8 g 7 t
ORIGIN
Query Match 0.68; Score 22; DB 6; Length 22;
Host Local Similarity 100.0%; Prod. No. 3,57;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2554 gccctctgagctcagctcagct 2575
DB 1 gccctctgagctcagctcagct 22

```

BASE COUNT 2 a 8 c 6 g 6 t  
ORIGIN

Query Match 0.6% Score 22 DB 6 Length 22  
Best Local Similarity 100.0% Pred. No. 3.5  
Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 724 attcagagcagctctctcc 745  
|||||  
Db 1 GCTGCAAGGAGGTCCTCTCC 22

RESULT 29  
LOCUS A78793 22 bp DNA PAT 19-OCT-1999  
DEFINITION Sequence 14 from patent EP0563714.  
ACCESSION A78793  
VERSION A78793.1 GI:6090189  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Lesslauer, W. and Loetscher, H.  
TITLE TNF-MUTAINS  
JOURNAL Patent: EP 0563714-A 14 05-OCT-1993;  
HOFFMANN LA FORTHE (CH)

FEATURES  
Location/Qualifiers  
1..22  
Source /organism="unidentified"  
/db\_xref="taxon:32944"

BASE COUNT 2 a 8 c 8 g 4 t  
ORIGIN

Query Match 0.6% Score 22 DB 6 Length 22  
Best Local Similarity 100.0% Pred. No. 3.5  
Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2231 gcctccctgagcagctctcc 2242  
|||||  
Db 1 GCTTCTTGCCATGCGCTGG 22

RESULT 30  
LOCUS AP052922 22 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 46 from patent US 5831976.  
ACCESSION AP052922  
VERSION AP052922.1 GI:5477784  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Maleyly, R. deWail, Howard, M., Hsu, D., Ishida, H., O'Garra, A.,  
Spits, H. and Zlotnik, A.  
TITLE Use of interleukin-10 (IL-10) to treat endotoxin- or  
superantigen-induced toxicity  
JOURNAL Patent: US 5831976-A 46 10-NOV-1998;  
FEATURES  
Location/Qualifiers  
1..22  
Source /organism="unknown"

BASE COUNT 3 a 8 c 5 g 6 t  
ORIGIN

Query Match 0.6% Score 22 DB 6 Length 22  
Best Local Similarity 100.0% Pred. No. 3.5  
Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2494 ctgagagagggagcagctctca 2515

|||||  
Db 22 CTGAGAGAGAGTCAGCTCA 1

RESULT 41  
LOCUS AK054285 22 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 46 from patent US 5837232.  
ACCESSION AK054285  
VERSION AK054285.1 GI:5979662  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)  
AUTHORS de Wail Maleyly, R., Howard, M., Hsu, D., Ishida, H., O'Garra, A.,  
Spits, H. and Zlotnik, A.  
TITLE Use of an interleukin-10 antagonist to treat a B cell mediated  
autoimmune disorder  
JOURNAL Patent: US 5837232-A 46 17-NOV-1998;  
FEATURES  
Location/Qualifiers  
1..22  
Source /organism="unknown"

BASE COUNT 3 a 8 c 5 g 6 t  
ORIGIN

Query Match 0.6% Score 22 DB 6 Length 22  
Best Local Similarity 100.0% Pred. No. 3.5  
Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2494 ctgagagagggagcagctca 2515  
|||||  
Db 22 CTGAGAGAGAGTCAGCTCA 1

RESULT 42  
LOCUS AK054487 22 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 46 from patent US 5837293.  
ACCESSION AK054487  
VERSION AK054487.1 GI:5980064  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)  
AUTHORS de Wail Maleyly, R., Howard, M., Hsu, D., Ishida, H., O'Garra, A.,  
Spits, H. and Zlotnik, A.  
TITLE Use of interleukin-10 antagonists for autoantibodies to treat endotoxin  
or superantigen-induced toxicity  
JOURNAL Patent: US 5837293-A 46 17-NOV-1998;  
FEATURES  
Location/Qualifiers  
1..22  
Source /organism="unknown"

BASE COUNT 3 a 8 c 5 g 6 t  
ORIGIN

Query Match 0.6% Score 22 DB 6 Length 22  
Best Local Similarity 100.0% Pred. No. 3.5  
Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2494 ctgagagagggagcagctca 2515  
|||||  
Db 22 CTGAGAGAGAGTCAGCTCA 1

RESULT 43  
LOCUS AR100414 22 bp DNA PAT 11-FEB-2001  
DEFINITION Sequence 44 from patent US 6080580.  
ACCESSION AR100414

REFERENCE: ROSEN, ROBERT SA (FRO)  
OTHER PUBLICATION: FR 2748032, 19971031.  
FEATURES  
SOURCE: 1. 29  
/organism "unidentified"  
/db\_xref "taxon:32644"

BASE COUNT: 6 a 11 c 0 g 12 t  
ORIGIN

Query Match: 0.6%; Score 23; DB 6; Length 29;  
Best Local Similarity: 100.0%; Pred. No. 0.94;  
Matches: 23; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY: 1224 taatgaatgaatgaatgaatga 1245  
|||||  
DB: 26 tcaatgaatgaatgaatgaatga 4

## RESULT 25

ALB754 22 bp DNA PAT 25 APR-1994  
LOCUS: A18754  
DEFINITION: oligonucleotide primer.  
ACCESSION: A18754  
VERSION: A18754.1 GI:514401  
KEYWORDS: synthetic construct;  
SYNOPSIS: synthetic construct  
ORIGIN: synthetic construct  
at the 1st sequence.

REFERENCE: 1 (bases 1 to 22)  
AUTHORS: FLORES, W.; FAVRENIER, J.; and VAN OSTADE, X.  
TITLE: TNP Motions  
JOURNAL: Patient: EP 0486938-A 7 27 MAY-1992;  
F. HOFFMANN LA ROCHE AG  
FEATURES  
SOURCE: 1. 22  
/organism "unidentified"  
/db\_xref "taxon:32644"

BASE COUNT: 2 a 8 c 8 g 4 t  
ORIGIN

Query Match: 0.6%; Score 22; DB 6; Length 22;  
Best Local Similarity: 100.0%; Pred. No. 3.5;  
Matches: 22; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY: 2221 taatgaatgaatgaatgaatga 2242  
|||||  
DB: 1 gggctgagggctgagggctgaggg 22

## RESULT 26

A09908 22 bp DNA PAT 05-MAR-1997  
LOCUS: A09908  
DEFINITION: Sequence 6 from Patient EP0619372.  
ACCESSION: A09908  
VERSION: A09908.1 GI:2296126  
KEYWORDS: unidentified;  
SYNOPSIS: unidentified;  
ORIGIN: unidentified;  
unclassified.

REFERENCE: 1 (bases 1 to 22)  
AUTHORS: BARNER, D.; JOESTLANDER, W.; JOESTLANDER, R.; and STUEBEL, D.  
TITLE: Tumor necrosis factor mutants  
JOURNAL: Patient: EP 0619372-A 6 12-OCT-1994;  
HOFFMANN LA ROCHE (CH)

COMMENT: other publication: EP 9405576, 950215  
other publication: JP 8009976, 960116  
other publication: CA 2119089, 940940  
other publication: AU 5901994, 941006  
other publication: CN 1099802, 950308  
other publication: RU 68218, 950628  
other publication: RU 263146, 951025

OTHER PUBLICATION: BR 9401421, 941018  
OTHER PUBLICATION: FI 941459, 940940  
OTHER PUBLICATION: NO 941142, 940940.  
FEATURES  
SOURCE: 1. 22  
/organism "unidentified"  
/db\_xref "taxon:32644"

BASE COUNT: 4 a 4 c 8 g 7 t  
ORIGIN

Query Match: 0.6%; Score 22; DB 6; Length 22;  
Best Local Similarity: 100.0%; Pred. No. 3.5;  
Matches: 22; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY: 2554 gattctggagctgattctgattctg 2575  
|||||  
DB: 1 gattctggagctgattctgattctg 22

## RESULT 27

A61448 22 bp DNA PAT 09-MAR-1998  
LOCUS: A61448  
DEFINITION: Sequence 7 from Patient W9970342  
ACCESSION: A61448  
VERSION: A61448.1 GI:3715850  
KEYWORDS: unidentified;  
SYNOPSIS: unidentified;  
ORIGIN: unidentified;  
unclassified.

REFERENCE: 1 (bases 1 to 22)  
AUTHORS: SCHMIDT, G.  
TITLE: CHIMERIC OLIGONUCLEOTIDES AND USES THEREOF IN THE IDENTIFICATION  
OF ANTIGEN BINDING SITES  
JOURNAL: Patient: WO 9710342-A 7 20-MAR-1997;  
BRAX GENOMICS LTD (GB)

FEATURES  
SOURCE: 1. 22  
/organism "unidentified"  
/db\_xref "taxon:32644"

BASE COUNT: 1 a 10 c 2 g 9 t  
ORIGIN

Query Match: 0.6%; Score 22; DB 6; Length 22;  
Best Local Similarity: 100.0%; Pred. No. 3.5;  
Matches: 22; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY: 888 gttctgagctgattctgattctg 909  
|||||  
DB: 1 gttctgagctgattctgattctg 22

## RESULT 28

A61444 22 bp DNA PAT 09-MAR-1998  
LOCUS: A61444  
DEFINITION: Sequence 13 from Patient W9710342.  
ACCESSION: A61444  
VERSION: A61444.1 GI:3715856  
KEYWORDS: unidentified;  
SYNOPSIS: unidentified;  
ORIGIN: unidentified;  
unclassified.

REFERENCE: 1 (bases 1 to 22)  
AUTHORS: SCHMIDT, G.  
TITLE: CHIMERIC OLIGONUCLEOTIDES AND USES THEREOF IN THE IDENTIFICATION  
OF ANTIGEN BINDING SITES  
JOURNAL: Patient: WO 9710342-A 13 20-MAR-1997;  
BRAX GENOMICS LTD (GB)

FEATURES  
SOURCE: 1. 22  
/organism "unidentified"  
/db\_xref "taxon:32644"

QY 594 ccagatgaactcagatgattcttcc 537  
 DB 24 CCAGATGACCTCATGCGATTTCGC 1

RESULT 20  
 LOCUS AX104832.7 24 bp DNA PAT 40-APR 2001  
 DEFINITION Sequence 1024 from Patent WO9122972.  
 ACCESSION AX104832  
 VERSION AX104832.1 GI:14921029  
 KEYWORDS

SOURCE  
 ORGANISM  
 REFERENCE  
 1 (bases 1 to 24)  
 AUTHORS Kriegl, A.M., Scheller, C., and Vollmer, J.C.  
 TITLE Immunostimulatory nucleic acids  
 JOURNAL Patent: WO 0122972-A 1024 05 APR 2001;  
 UNIVERSITY OF LEINA RESEARCH INSTITUTION (US) ; GARY PLATTENBERG

FEATURES  
 source  
 1..24  
 /organism="Synthetic construct"  
 /db\_xref="taxon:32630"  
 BASE COUNT 7 a 6 c 7 g 4 t  
 ORIGIN

Query Match 0.7% Score 24; DB 6; Length 24;  
 Best Local Similarity 100.0%; Prod. No. 9.26;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 504 ccagatgaactcagatgattcttcc 537  
 DB 24 CCAGATGACCTCATGCGATTTCGC 1

RESULT 21  
 LOCUS 139730 24 bp DNA PAT 13 MAY 1997  
 DEFINITION Sequence 3 from patent US 5616490.  
 ACCESSION 139730  
 VERSION 139730.1 GI:2084210  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 1 (bases 1 to 24)  
 AUTHORS Sullivan, S.M., and Harper, K.J.  
 TITLE Ribozymes targeted to TNF- $\alpha$  RNA  
 JOURNAL Patent: US 5616490-A 3 01-APR-1997;  
 FEATURES  
 source  
 1..24  
 /organism="unknown"  
 BASE COUNT 8 a 11 c 3 g 2 t  
 ORIGIN

Query Match 0.7% Score 24; DB 6; Length 24;  
 Best Local Similarity 100.0%; Prod. No. 9.26;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 605 ccagatgaactcagatgattcttcc 708  
 DB 1 CCGCTCAAAACACCCCAACGCG 24

RESULT 22  
 LOCUS AX012485 24 bp RNA PAT 06 SEP 2000  
 DEFINITION Sequence 1 from Patent WO9954449.

ACCESSION AX012485  
 VERSION AX012485.1 GI:9998484  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 1 (bases 1 to 23)  
 AUTHORS Harvey, W.  
 TITLE Method of analysis of chronic wounds  
 JOURNAL Patent: WO 99/4432 A 1 28 SEP 1999;  
 UNIVERSITY OF MARYLAND MEDICAL CENTER (US); HARVEY WILSON N (US)  
 FEATURES  
 source  
 1..23  
 /organism="Synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Primer used in analysis for TNF- $\alpha$ "

BASE COUNT 6 a 2 c 9 g 6 t  
 ORIGIN

Query Match 0.4% Score 23; DB 6; Length 24;  
 Best Local Similarity 100.0%; Prod. No. 9.94;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 284 agcgaatgaatttttgaagat 306  
 DB 1 AGCGAATGAGTTTGGGCGGAT 24

RESULT 23  
 LOCUS 139736 23 bp DNA PAT 13 MAY 1997  
 DEFINITION Sequence 9 from patent US 5616490.  
 ACCESSION 139736  
 VERSION 139736.1 GI:2084216  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 1 (bases 1 to 23)  
 AUTHORS Sullivan, S.M., and Harper, K.J.  
 TITLE Ribozymes targeted to TNF- $\alpha$  RNA  
 JOURNAL Patent: US 5616490-A 9 01-APR-1997;  
 FEATURES  
 source  
 1..23  
 /organism="unknown"  
 BASE COUNT 1 a 8 c 5 g 9 t  
 ORIGIN

Query Match 0.4% Score 23; DB 6; Length 24;  
 Best Local Similarity 100.0%; Prod. No. 9.94;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 881 gattgatttctcagctcttc 904  
 DB 1 GGTGCTTGTTGTCAGGCTCTTC 24

RESULT 24  
 LOCUS Ab6669 23 bp RNA PAT 29 MAR 1999  
 DEFINITION Sequence 11 from Patent WO9719172.  
 ACCESSION Ab6669  
 VERSION Ab6669.1 GI:1528159  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 1 (bases 1 to 29)  
 AUTHORS Mallet, J.C., Molodt, R., Ravassard, P., and Leclercq, F.  
 TITLE DERIVED TYPE-III HYDROLYTIC GENE EXPRESSION SYSTEM  
 JOURNAL Patent: WO 9740172-A 14 03-0CT-1997;

TITLE: TTP related zinc finger domains and methods of use  
 Patent: WO 01/22972-A 1: 22 FEB 2001;  
 THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

## FEATURES

## SOURCE

Location/Qualifiers

BASE COUNT 6 a 0 c 0 g 18 t

## ORIGIN

Query Match 0.78; Score 24; 18 b; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.26;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 TTAATTATTAATTATTAATTATTT 24

## RESULT 16

## AX103940

LOCUS 24 bp DNA PAT 40-APR-2001  
 DEFINITION Sequence 132 from Patent WO 01/22972.  
 ACCESSION AX103940  
 VERSION AX103940.1 GI:13920137

## KEYWORDS

## SOURCE

synthetic construct,  
 artificial sequence,  
 1 (bases 1 to 24)

## REFERENCE

## AUTHORS

Krivan, A.M., Schetter, C., and Vollmer, J.C.,  
 Immunosimulatory nucleic acids

## TITLE

Patent: WO 01/22972-A 1: 22 FEB 2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical

## JOURNAL

Gmbh (DE)

## FEATURES

Location/Qualifiers

## BASE COUNT

1. 24  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630" 6 t

## ORIGIN

Query Match 0.78; Score 24; 18 b; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.26;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 CGAGTTCGACATGACGTCATG 24

## RESULT 17

## AX103941

LOCUS 24 bp DNA PAT 40-APR-2001  
 DEFINITION Sequence 134 from Patent WO 01/22972.  
 ACCESSION AX103941  
 VERSION AX103941.1 GI:13920138

## KEYWORDS

## SOURCE

synthetic construct,  
 artificial sequence,  
 1 (bases 1 to 24)

## REFERENCE

## AUTHORS

Krivan, A.M., Schetter, C., and Vollmer, J.C.,  
 Immunosimulatory nucleic acids

## TITLE

Patent: WO 01/22972-A 1: 22 FEB 2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical

## JOURNAL

Gmbh (DE)

## FEATURES

Location/Qualifiers

## SOURCE

1. 24  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630" 6 t

BASE COUNT 6 a 5 c 9 g 4 t

## ORIGIN

Query Match 0.78; Score 24; 18 b; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.26;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 CGGCTTCGACATGACGTCATG 1

## RESULT 18

## AX103942

LOCUS 24 bp DNA PAT 40-APR-2001  
 DEFINITION Sequence 134 from Patent WO 01/22972.  
 ACCESSION AX103942  
 VERSION AX103942.1 GI:13920139

## KEYWORDS

## SOURCE

synthetic construct,  
 artificial sequence,  
 1 (bases 1 to 24)

## REFERENCE

## AUTHORS

Krivan, A.M., Schetter, C., and Vollmer, J.C.,  
 Immunosimulatory nucleic acids

## TITLE

Patent: WO 01/22972-A 1: 22 FEB 2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical

## JOURNAL

Gmbh (DE)

## FEATURES

Location/Qualifiers

## BASE COUNT

1. 24  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630" 7 t

## ORIGIN

Query Match 0.78; Score 24; 18 b; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.26;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 CGAGTTCGACATGACGTCATG 24

## RESULT 19

## AX103943

LOCUS 24 bp DNA PAT 40-APR-2001  
 DEFINITION Sequence 135 from Patent WO 01/22972.  
 ACCESSION AX103943  
 VERSION AX103943.1 GI:13920140

## KEYWORDS

## SOURCE

synthetic construct,  
 artificial sequence,  
 1 (bases 1 to 24)

## REFERENCE

## AUTHORS

Krivan, A.M., Schetter, C., and Vollmer, J.C.,  
 Immunosimulatory nucleic acids

## TITLE

Patent: WO 01/22972-A 1: 22 FEB 2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical

## JOURNAL

Gmbh (DE)

## FEATURES

Location/Qualifiers

## BASE COUNT

1. 24  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630" 4 t

## ORIGIN

Query Match 0.78; Score 24; 18 b; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.26;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







BASE COUNT 6 a 7 c 10 d 7 t  
ORIGIN

Query Match 0.88; Score 30; DB 6; Length 40;  
Best Local Similarity 100.0%; Prod. No. 0.0001;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2756 ccctgagatcagaagaatgagcctgagca 2785  
Db 1 CCTGGAGATCAGGAATGAGCCTGAGCA 30

RESULT 2  
LOCUS 139759 29 bp UNA  
DEFINITION Sequence 32 from patent US 5616490  
ACCESSION 139759  
VERSION 139759.1 GI:2084239  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Sullivan, S.M. and Draper, K.G.  
TITLE Ribozymes targeted to TNF- $\alpha$ . RNA  
JOURNAL Patent: US 5616490-A 32 01-APR-1997;  
FEATURES  
Source location/Qualifiers  
I. 29  
/organism="unknown"

BASE COUNT 6 a 8 c 9 g 6 t  
ORIGIN

Query Match 0.88; Score 29; DB 6; Length 29;  
Best Local Similarity 100.0%; Prod. No. 0.00048;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3129 gacccatgtagagcctgctgctgacg 3157  
Db 1 GACCCATGTAGAGCCTGCTGCTGACG 29

RESULT 3  
LOCUS 139731 28 bp DNA  
DEFINITION Sequence 4 from patent US 5616490  
ACCESSION 139731  
VERSION 139731.1 GI:2084211  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Sullivan, S.M. and Draper, K.G.  
TITLE Ribozymes targeted to TNF- $\alpha$ . RNA  
JOURNAL Patent: US 5616490-A 4 01-APR-1997;  
FEATURES  
Source location/Qualifiers  
I. 28  
/organism="unknown"

BASE COUNT 7 a 11 c 7 g 3 t  
ORIGIN

Query Match 0.88; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Prod. No. 0.0014;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 709 cacatccctgacaagctgcacagcag 736  
Db 1 CACATCCCTGACAAGCTGCACAGCAG 28

RESULT 4  
LOCUS 139753 27 bp UNA  
DEFINITION Sequence 26 from patent US 5616490.  
ACCESSION 139753  
VERSION 139753.1 GI:2084233  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Sullivan, S.M. and Draper, K.G.  
TITLE Ribozymes targeted to TNF- $\alpha$ . RNA  
JOURNAL Patent: US 5616490-A 26 01-APR-1997;  
FEATURES  
Source location/Qualifiers  
I. 27  
/organism="unknown"

BASE COUNT 11 a 7 c 4 g 5 t  
ORIGIN

Query Match 0.78; Score 27; DB 6; Length 27;  
Best Local Similarity 100.0%; Prod. No. 0.0051;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2923 agactgactgaatgaaatgaaatgaaat 2949  
Db 1 AGACTGACTGAATGAAATGAAATGAA 27

RESULT 5  
LOCUS E21959/c 26 bp DNA  
DEFINITION Method for assaying nucleic acid and reagent therefor.  
ACCESSION E21959  
VERSION 1 GI:18023769  
KEYWORDS JP 1999032799-A/8.  
SOURCE unidentified.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Michio, S.K.I.T. and Itagaki, H.I.  
TITLE Method for assaying nucleic acid and reagent therefor  
JOURNAL Patent: JP 1999032799-A 8 09-FEB-1999;  
COMMENT  
OS unidentified  
PB JP 1999032799 A/8  
PD 09-FEB-1999  
PE 17-JUL-1997 JP 1997192824  
PK  
PL  
PT 179918023769 A/8 09-FEB-1999  
QC Strandedness: Single  
CT Topology: Linear  
FC Key  
FT source  
TT location/Qualifiers  
I. 26  
/organism="unidentified"

BASE COUNT 5 a 9 c 5 g 7 t  
ORIGIN

Query Match 0.78; Score 26; DB 6; Length 26;  
Best Local Similarity 100.0%; Prod. No. 0.019;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2765 caggaatgtatgctgacacatgaa 2790  
Db 26 CAGGAATGTATGCTGACACATGAA 1







PR 17-JUN-1992: 920S-0916763  
 PR 07-DEC-1992: 920S-0367132  
 PR 07-DEC-1992: 920S-0989848  
 PR 07-DEC-1992: 920S-0989849  
 PR 19-JAN-1993: 930S-0008895  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PI Draper KG, Sullivan SM  
 XX  
 DR WPI: 1994-04853/06.  
 XX  
 PT Biozymatic RNA molecules which cleave mRNA - used to treat or  
 prevent a fibrotic, asthmatic, chronic or cardiovascular disease  
 or conditions  
 XX  
 PS Claim 3: Page 16; 65pp; English.  
 XX  
 CC This is a 19F-alpha mRNA target sequence (nucleotide no. 1197) of an  
 CC enzymatic RNA molecule (ribozyme) which cleaves mRNA associated with  
 CC the development or maintenance of a psoriatic or asthmatic condition.  
 CC The concn. of the ribozyme necessary to effect a therapeutic treatment  
 CC is lower than that of an antisense oligonucleotide and the specificity  
 CC of action is higher.  
 CC  
 SU Sequence 26 BP: 7 A; 5 G; 9 G; 5 T; 0 other;  
  
 Query Match 0.78; Score 26; DB 15; Length 26;  
 Best Local Similarity 100.0%; Prod. No. 1.3;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Q7 2897 TGGTGGATTTGCTGCAATGCTTATGA 2922  
 Db 1 TGGCTGATGCTGCAAGACTTATGA 26  
  
 RESULT 22  
 AAT76392/c  
 ID AAT76392 standard; DNA: 26 BP.  
 AC AAT76392:  
 XX  
 DT 15-SEP-1997 (first entry)  
 XX  
 DE Human tumour necrosis factor alpha antisense oligonucleotide H51NFAAS11.  
 XX  
 KW Asthma; airway epithelium; adenosine free; cystic fibrosis;  
 KW chronic obstructive pulmonary disease; bronchitis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W09640162-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PE 06-JUN-1996; 96W0-0509406.  
 XX  
 PR 07-JUN-1995; 95US-0474497.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PI Metzger WJ, Ryce JW;  
 XX  
 DR WPI: 1997-051871/05.  
 XX  
 PT Treatment of airway diseases such as asthma - by topically applying  
 PT adenosine-free antisense oligonucleotide to airway epithelium of  
 P1 subject  
 XX  
 PS Claim 5; Page 37; 71pp; English.  
 CC A method for treating airway disease in a subject has been provided.

CC which involves the topical administration of an essentially adenosine  
 CC free antisense oligonucleotide (96) to the airway epithelium of the  
 CC subject. The present sequence is an antisense oligonucleotide  
 CC H51NFAAS11 effective for the human tumour necrosis factor alpha. The  
 CC method can be used to treat airway diseases such as cystic fibrosis,  
 CC asthma, chronic obstructive pulmonary disease, bronchitis and other  
 CC airway diseases characterized by an inflammatory response. By  
 CC eliminating adenosine from the antisense ON, its interaction upon  
 CC antisense degradation is prevented, thereby providing adenosine  
 CC induced bronchoconstriction in patients with hyper-reactive airways.  
 CC  
 SU Sequence 26 BP: 0 A; 10 G; 5 C; 11 T; 0 other;  
  
 Query Match 0.78; Score 26; DB 15; Length 26;  
 Best Local Similarity 100.0%; Prod. No. 1.3;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Q7 2055 GACAGATGATGATGATGATGATGATGATGAT 2080  
 Db 26 GACAGATGATGATGATGATGATGATGATGAT 1  
  
 RESULT 23  
 AAX58199  
 ID AAX58199 standard; DNA: 26 BP.  
 AC AAX58199:  
 XX  
 DT 21-JUL-1999 (first entry)  
 XX  
 DE Primer for Gadd-45 fusion protein construction.  
 XX  
 KW Gadd-45 fusion protein; erythropoietin receptor dimerisation domain;  
 KW protein-protein interaction; periplasmic domain; transmembrane domain;  
 KW Gadd-45 transcriptional regulatory domain; receptor interaction;  
 KW ligand identification; orphan receptor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W09923116-A1.  
 XX  
 PD 14-MAY-1999.  
 XX  
 PE 03-NOV-1998; 98W0-0523307.  
 XX  
 PR 09-SEP-1998; 98US-0149922.  
 PR 03-NOV-1997; 97US-0064058.  
 XX  
 PA (SMAL-) SMALL MOLECULE THERAPEUTICS INC.  
 XX  
 PI Hsing W, Menzel K, Taggart PA;  
 XX  
 DR WPI: 1999-41305/26.  
 XX  
 New Gadd-45 fusion polypeptide nucleic acid constructs  
 Example: Page 88; 124pp; English.  
  
 CC This sequence represents a PCR primer used in the construction of a  
 CC Gadd-45 fusion polypeptide.  
 CC The invention relates to Gadd-45 fusion polypeptide nucleic acid constructs  
 CC which are used to transform cells to produce systems for identifying  
 CC compounds which modulate interactions between protein sequences. The  
 CC Gadd-45 fusion polypeptides comprise a periplasmic domain, a transmembrane  
 CC domain and a Gadd-45 transcriptional regulatory domain. Cells transformed  
 CC with nucleic acid encoding the fusion proteins and a Gadd-45 reporter  
 CC construct can be used for identifying compounds which modulate a specific  
 CC protein-protein interaction such as modulation of interactions between  
 CC protein sequences involved in receptor interactions, e.g. dimerisation.  
 CC Such methods can be used for identifying ligands for orphan receptors.  
 CC The system is extremely sensitive in that background is low and the  
 CC magnitude of signal background is five to ten fold greater than that even minor















KW	cancer-abstract-two pulmonary disease; pulmonary infection; bronchitis
KM	cancer-ss.
XX	
OS	Bromo scriptions
PN	We2000b6.27.66 A.Z.
XX	
PD	.26 oct. 2000 .
XX	
PE	24 MAR 2000; 2000QWO USOH020.
XX	
PR	06 APR 1999; 9908S-01.2790H.
XX	
PA	(UNIV.) UNIV EAST CAROLINA,
XX	(NOV?) NOV J W.
PL	Nylon JW;
XX	
DIR	MPI: 2000 6705.ty766.
PT	low adenosine (A) content and isense of ligand-foot lids which do not
PT	tougher adenosine receptor as during metabolism, usual e.g. for treating
PT	cancers and respiratory disorders -
PS	claim 14; Page 241; 1542pp; English.
XX	
CC	The present invention describes low adenosine (A) content and isense
CC	of ligand-foot lids and compositions (I) comprising them. In the isense
CC	of footbed lids the A is replaced by a "theoretical or alternative base"
CC	(I) can have respiratory, proinflammatory, and inflammatory analgesic,
CC	immunosuppressive, and vasodilatory hypotensive and cyclooxygenase activities.
CC	The ant isense of ligandfoot lids and (I) can be used to down-regulate the
CC	expression and/or activity of target polypeptides associated with
CC	lung/respiratory disorders and inflammations, such as stimulating and
CC	activating pituitary factors and neurotransmitters, transcription factors,
CC	immunoglobulins and antibodies, antibody receptors, cytokines and
CC	chemokines, endogenously produced specific and non-specific enzymes,
CC	binding proteins, adhesion molecules and their receptors, cytokine and
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central
CC	nervous system (CNS) and peripheral nervous and non-nervous system pain
CC	receptors, CNS and peripheral nervous and non-nervous system peptide
CC	transmitters, detoxifiers, growth factors, cytochrome peptides and
CC	receptors, binding proteins and metalloproteins associated proteins. The
CC	ant isense of ligandfoot lids may be used in this way to treat disorders
CC	Including respiratory obstruction (especially pulmonary obstruction
CC	and/or bronchoconstriction), asthma, lung edema, etc., all of which are
CC	and/or surface and hypersecretion which are associated with a disease or
CC	condition selected from pulmonary vasoconstriction, inflammation,
CC	allergic asthma, impaired respiration, respiratory distress syndrome
CC	(RDS), pain, cystic fibrosis (CF), alveolar thinitis (AA), pulmonary
CC	bypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC	dust/allergy, AAPB444 to AAP21543 represent human poly nucleotide
CC	fragments and ant isense of ligandfoot lids used in the exemplification of
CC	the present invention.
XX	
NO	Sequence 25: bp; 0 A; 12 G; 7 C; 6 T; 0 other;
UY	Curey Match                  0.78; Score 25; BH 21; Length 25;
UY	Best Local Similarity 100.0%; Prod. No. 8.4;
Matches	25; Conserved too; n; Mismatched o; Indels o; Gaps
YY	2420 acacatcttttgcgcaaacgaagcggcggttc 2444   db 25 gctaccacaaagcccccacacacaaaac 1
RESULT 47	
AAA00874	
ID	AAA00874 standard; DNA; 25 bp;
NC	AAA00874:

	XX	Z1- <b>FEB8-2001</b> (first entry)
DJ	XX	
DE	XX	Human Tumour necrosis factor alpha promoter beta site probe #1.
EE	XX	Human; TNFalpha; Tumour necrosis factor alpha; promoter; beta site;
KW	XX	DNA binding protein; inflammatory disease; probe; ds.
OS	XX	Homo sapiens.
XN	XX	
FN	XX	M0200047768-AI.
PD	XX	17-Aug-2000.
DP	XX	09-FEB-2000; 2000WO-GH00414.
RK	XX	09-FEB-1999; 99GB-000Z919.
EY	XX	(EST) NCBI ENTREZGEN LTD.
JL	XX	Katoh H.; Katkowski DP;
BX	XX	WPt_2000-579935754.
PT	XX	Sequence specific DNA binding protein capable of binding specifically to the alpha site human tumor necrosis factor alpha promoter useful for identifying compounds which can modulate the expression of tumor necrosis factor-alpha
BS	XX	claim 28; Page 7; 50pp; English.
CQ	XX	The present sequence is a probe used to detect the beta site of the human necrosis factor alpha (TNF alpha) promoter sequences. The probe can be used to identify DNA-binding proteins and compounds which interfere with the normal transcription factor binding at this position, enabling the modulation of TNF alpha gene expression. The alpha site, which is also a feature of the invention, contains a polymorphism, the sequence of which can be used to test an individual's predisposition to inflammatory diseases. These include cerebral malaria, rheumatoid arthritis, familial celiac disease and cystic fibrosis before cryotherapeutics.
SZ	XX	sequence 25 bp: T A G C G G G G 2 T 0 other:
GZ	XX	
BC	XX	Query Match: 67% Score 25; PB 21; Length 25; Best local similarity: 136.0%; Pval: No; 3 k; Mismatch: 2; Count after: 0; Mismatches: 0; Indels: 0; gaps: 0;
OJ	XX	21c tatattgatactacactacaatga tgg 
LH	XX	t tataaaagaaa aaaga acacacac 25
FE	XX	
FI	XX	RESULT 38
ID	XX	AAA90R96
AA	XX	AAA90R96 standard; DNA: 25 BP.
AC	XX	AAA90R96;
AT	XX	21-FEB-2001 (first entry)
BE	XX	Human tumou necrosis factor alpha promoter beta site EMCA probe #2.
KM	XX	Humano; TNFalpha; Tumour necrosis factor alpha; promoter; beta site;
KW	XX	DNA binding protein; inflammatory disease; probe; ss.
OS	XX	Homo sapions.
PN	XX	M0200047768-AI.
PD	XX	17-Aug-2000
PF	XX	09-FEB-2000; 2000WO-GH00414.

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XX 06-FEB-1999: 646R-0002919
XX (ISIS-) ISIS INNOVATION LTD.
XX Knight JC, Kwiatkowski DP;
XX WPI: 2000-579035/54
XX Sequence specific DNA binding protein capable of binding specifically
XX to the alpha site human tumor necrosis factor-alpha promoter useful for
XX identifying compounds which can modulate the expression of tumor
XX necrosis factor-alpha
XX Example 3: Fig 7: 56pp; English.
XX The present sequence is a probe used to detect the position of the beta
XX site of the tumor necrosis factor-alpha (TNF-alpha) promoter sequence.
XX The alpha site, which is a part of the invention, contains a
XX polymorphism, the sequence of which can be used to test an individual's
XX predisposition to inflammatory diseases. These include cerebral malaria,
XX rheumatoid arthritis, inflammatory bowel disease and systemic lupus
XX erythematosus. The present sequence can also be used to identify
XX DNA-binding proteins and compounds which interfere with the normal
XX transcription factor binding at this position, enabling the regulation of
XX TNF-alpha gene expression. This probe was used in an electrophoretic
XX mobility shift assay to determine the precise position of the beta site.
XX Sequence 25 BP: 11 A; 6 G; 6 G; 2 T; 0 other;
XX
XX Query Match: 0.7%; Score 25; DB 21; Length 25;
XX Host Local Similarity 100.0%; Pred. No. 3.4;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 242 tagaaggaatcagacacagacacg 266
XX 1 tagaaggaatcagacacagacacg 25
XX
XX RESULT 39
XX AAC61633
XX ID AAC61633 standard; DNA: 25 BP.
XX AAC61633;
XX 19-FEB-2001 (first entry)
XX PCR primer used to amplify a tumour necrosis factor alpha gene.
XX Human: tumour necrosis factor alpha; biorecognition microchip;
XX single nucleotide polymorphism, TCF primer, ss.
XX Homo sapiens.
XX W0209058522-A1.
XX 05-OCT-2000.
XX 29-MAR-2000; 200006-759077
XX 30-MAR-1999; 9905-0126865.
XX (NANO-) NANOGEN INC.
XX Giles PM, Dillon PJ, Wu DJ, Foster CB, Chanock SJ;
XX WPI: 2000-638454/61
XX Detecting single nucleotide polymorphism by utilizing a bioelectronic
XX microchip having several test sites
XX Example 4; Page 17; 46pp; English.

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XX PCR primer AAC61633 used to amplify a tumour necrosis factor
XX alpha gene. The method of the invention was used for detecting single
XX nucleotide polymorphisms (SNPs) in the tumour necrosis factor alpha
XX gene. The method utilizes electronic circuitry on silicon microchips.
XX The method provides accurate discrimination of amplified DNA samples
XX following electrophoretic transport, concentration, and attachment of DNA to
XX selected electrodes (test sites). The test sites make up or include
XX arrays of samples that are distinguished by using internal controls of
XX dual labeled reporters comprising wild type and mismatched sequences to
XX validate the SNP genotype. Multiples of SNPs in target nucleotide acids
XX from a patient sample source or a SNP in target nucleotide acids of
XX multiple patient sample sources can also be detected using the
XX electronically addressable microchip.
XX Sequence 25 BP: 11 A; 6 G; 6 G; 2 T; 0 other;
XX
XX Query Match: 0.7%; Score 25; DB 21; Length 25;
XX Host Local Similarity 100.0%; Pred. No. 3.4;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 242 tagaaggaatcagacacacacg 264
XX 1 tagaaggaatcagacacacacg 25
XX
XX RESULT 40
XX AAA65278
XX ID AAA65278 standard; DNA: 25 BP.
XX AAA65278;
XX 07-NOV-2000 (first entry)
XX Tumour necrosis factor activation factor oligonucleotide #3.
XX High throughput assay system, mass spectrometry, 13 bp, anchor;
XX linker detection; protection; identification screening;
XX genetic mutation; pathogen; gene expression; ss.
XX Synthesis.
XX W200007684-A1.
XX 29-JUN-2000.
XX 22-DEC-1999; 99W0-0530515.
XX 22-DEC-1998; 9805-0218166.
XX (Kb-S/) KGIS R M.
XX (PELN/) PELEDER S.
XX KGIS RM, Felder S;
XX WPI: 2000-442695/48.
XX Detecting nucleic acids useful for drug screening and studying gene
XX expression. The method comprises subjecting a sample containing the
XX nucleic acids to nucleic acid protection with one or more protection
XX fragments and detecting the hybridized duplex molecules, or the single
XX stranded nucleic acids or protection fragments with mass spectrometry.
XX The method is useful for detecting one or more targets or nucleic acids
XX in a sample. The method therefore has applications in screening for
XX peptides or potential drugs which bind a receptor of interest, for
XX screening for the presence of nucleic mutations or for pathogens or for

```

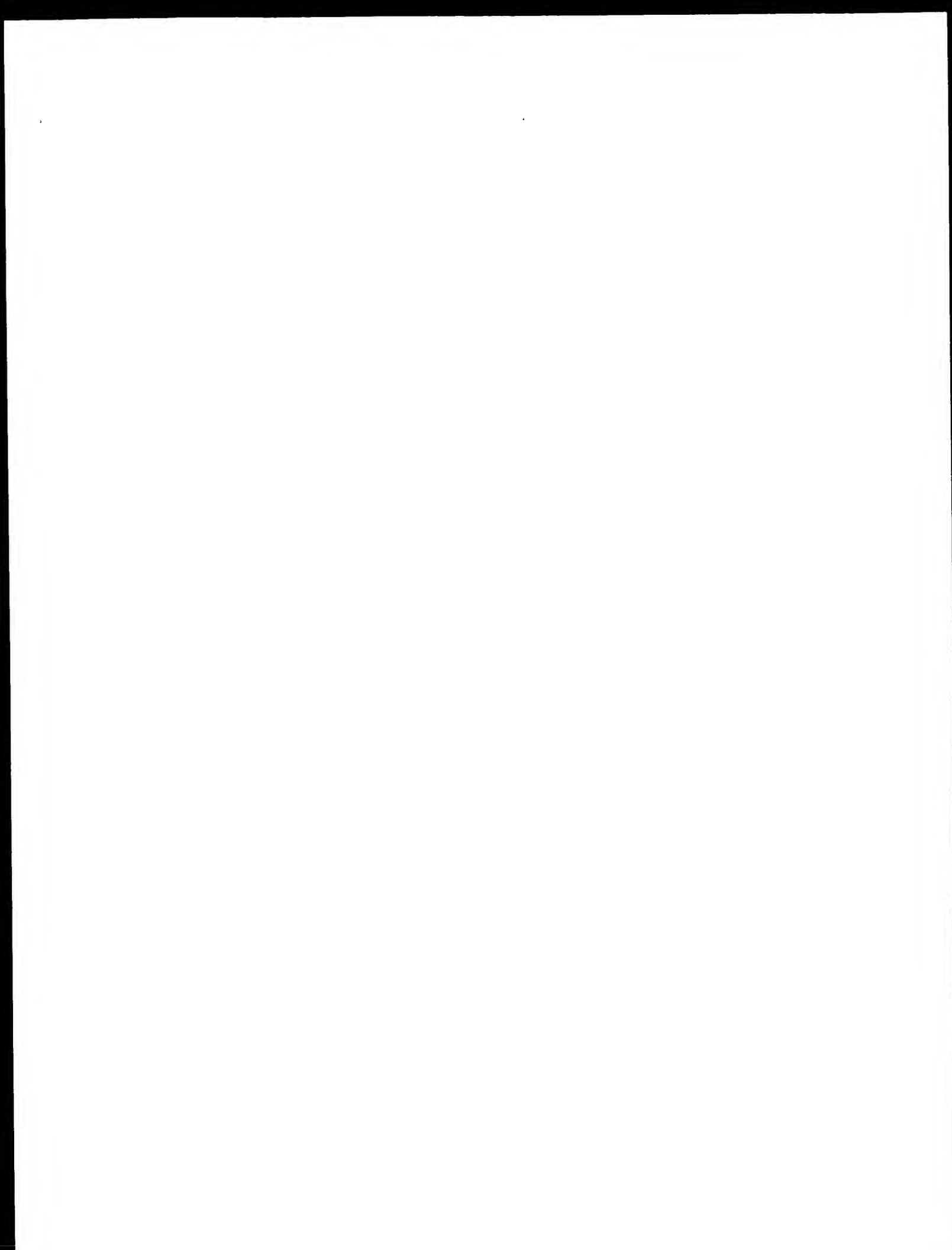












GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2002, 03:22:03, Search time: 200.95 Seconds

(without alignments)  
13210.607 Million cells 341105/500

Title: US-09-824-322B-1

Perfect score:

3634

Sequence:

1 gaattcggatgatttact.....attcgaactctgaattc 3634

Scoring table:

01100\_MNC  
Gapop 60 0 0 Gapext 60 0 0

Searched:

1151937 seqs, 537289281 residues

Word size:

0

Total number of hits satisfying chosen parameters:

25812

Minimum DB seq length:

3

Maximum DB seq length:

30

Post-processing: Listing first 45 summaries

Database:

EST:  
1: em\_estfun:  
2: em\_esthum:  
3: em\_estin:  
4: em\_estom:  
5: em\_estopl:  
6: em\_estba:  
7: em\_estro:  
8: em\_estov:  
9: em\_hic:  
10: qb\_est1:  
11: qb\_est2:  
12: qb\_hic:  
13: qb\_gss:  
14: em\_gssfun:  
15: em\_gsshum:  
16: em\_gssinv:  
17: em\_gsspin:  
18: em\_gsspro:  
19: em\_gssrod:  
20: em\_gssvrt:  
21: em\_gss\_other:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No	Score	Query Match	Length DB	ID	Description
1	19	0.5	25	12	AE666829 IM0519217
2	18	0.5	26	12	AE416392
3	17	0.5	23	13	AE430288 IM0214012
4	17	0.5	25	13	AE333212 IM0062911
5	16	0.4	22	13	AE854229 IM0157014
6	16	0.4	23	13	AE766246
7	15	0.4	25	11	180419 yd17311.s1
8	15	0.4	25	13	AE331633 IM0059811
9	15	0.4	25	13	AE345569 IM0080118
10	15	0.4	28	13	AE345640 IM0080134
11	15	0.4	28	13	AE328669 IM0212011
12	15	0.4	29	13	AE804183

13	14	0.4	19	13	AE333223	AE333223 IM0062908
14	14	0.4	20	11	AE11208	AE11208 HOM0290423
15	14	0.4	22	13	AE11494	AE11494 IM0270011
16	14	0.4	23	13	AE11446	AE11446 IM0563008
17	14	0.4	25	13	AE328635	AE328635 IM0052821
18	14	0.4	25	13	AE345473	AE345473 IM0080408
19	14	0.4	25	13	AE641910	AE641910 IM0504809
20	14	0.4	25	13	AE640938	AE640938 IM0138810
21	14	0.4	27	13	AE416143	AE416143 IM0191314
22	14	0.4	27	13	AE782295	AE782295 IM0059019
23	14	0.4	27	13	AE942892	AE942892 IM02024803
24	14	0.4	27	13	AE942892	AE942892 IM02024804
25	14	0.4	28	13	AE56764	AE56764 IM0524905
26	14	0.4	28	13	AE783984	AE783984 IM0020807
27	14	0.4	29	13	AE439429	AE439429 IM0229822
28	14	0.4	29	13	AE439429	AE439429 IM0065016
29	14	0.4	19	13	AE368047	AE368047 IM001012
30	14	0.4	19	13	AE430106	AE430106 IM0231304
31	14	0.4	19	13	AE489586	AE489586 IM0320112
32	14	0.4	19	13	AE510952	AE510952 IM0356315
33	14	0.4	19	13	AE983014	AE983014 IM0264002
34	14	0.4	20	13	AE433566	AE433566 IM0219092
35	14	0.4	20	13	AE152357	AE152357 IM0327824
36	14	0.4	20	13	AE508772	AE508772 IM0339815
37	14	0.4	20	13	AE725557	AE725557 IM0572808
38	14	0.4	21	13	AE413684	AE413684 IM0030008
39	14	0.4	21	13	AE394677	AE394677 IM0158624
40	14	0.4	21	13	AE394697	AE394697 IM0158811
41	14	0.4	21	13	AE503574	AE503574 IM0343819
42	14	0.4	21	13	AE589098	AE589098 IM0437819
43	14	0.4	21	13	AE627978	AE627978 IM0476104
44	14	0.4	21	13	AE926429	AE926429 IM0251924
45	14	0.4	22	10	AE014510	AE014510 AE014510

#### ALIGNMENTS

RESULT 1	25 bp	UNA	GNS	14 (98%-2000)
AE666829	IM0519217	Mouse 10kb plasmid 1000716	1000716	Mouse genomic
DEFINITION	clone: U00C1M05490C17 F1 DNA sequence.			
ACCESSION	AE666829			
VERSION	AE666829.1	GI:11803975		
KEYWORDS	GNS:			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryotic Metazoa: Chordata: Craniata: Vertebrata: Euplosteomi:			
AUTHORS	Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.			
	1 (bases 1 to 25)			
	Hum, D., Ayala, A., Hartoe, M., Pasavita, J., Peral, R., Ramil, C.,			
	Tejedor, J., Zeborova, K., Kalmus, M., Monedero, J., Pedersen, J., Seilly			
	M., Page, M., Wase, K., Stokoe, P., Hickey, A., von Norderhausen, A.			
	and Wright, D., Weiss, R.			
	Mouse whole genome scaffolding with paired end reads from 10kb			
	plasmid inserts			
	Unpublished (2000)			
JOURNAL	Contact: Robert B. Weiss			
COMMENT	University of Utah			
	84112, USA			
	TEL: 801 585 5606			
	FAX: 801 585 3127			
	Email: adunogenetics.utah.edu			
	Insert location: 1000716 and Error: 0.00			
	Plasmid: 6549 base, 6 columns, 17			
	Seq primer: GGTGTAAACACGACGACAT			
	Class: Plasmid ends			
FEATURES	High quality sequence stop: 25.			
Score	100.00/Qualifiers			
	1.25			



FEATURES

Location/Qualifiers

1..23  
/organism="Mus musculus"  
/strain="05781/61"

1..25  
/organism="Mus musculus"  
/strain="05781/61"

High quality sequence slope: 25.  
Location/Qualifiers

1..25  
/organism="Mus musculus"  
/strain="05781/61"

1..25  
/organism="Mus musculus"  
/strain="05781/61"

BASE COUNT

0 a 10 c 0 g 13 t

0 a 10 c 0 g 13 t

0 a 10 c 0 g 13 t

0 a 10 c 0 g 13 t

0 a 10 c 0 g 13 t

0 a 10 c 0 g 13 t

QUERY

1153 aagagagagagagagag 1169

1153 aagagagagagagagag 1169

1153 aagagagagagagagag 1169

1153 aagagagagagagagag 1169

1153 aagagagagagagagag 1169

1153 aagagagagagagagag 1169

1153 aagagagagagagagag 1169

RESULT

4  
A2333213

25 bp ENA

25 bp ENA

25 bp ENA

25 bp ENA

25 bp ENA

25 bp ENA

LOCUS

100.0% Identical

100.0% Identical

100.0% Identical

100.0% Identical

100.0% Identical

100.0% Identical

100.0% Identical

DEFINITION

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

ACCESSION

A2333213

A2333213

A2333213

A2333213

A2333213

A2333213

A2333213

VERSION

1

1

1

1

1

1

1

KEYWORDS

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

SOURCE

house mouse

house mouse

house mouse

house mouse

house mouse

house mouse

house mouse

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathia; Muridae; Mus; 1 (bases 1 to 25)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathia; Muridae; Mus; 1 (bases 1 to 25)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathia; Muridae; Mus; 1 (bases 1 to 25)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathia; Muridae; Mus; 1 (bases 1 to 25)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathia; Muridae; Mus; 1 (bases 1 to 25)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathia; Muridae; Mus; 1 (bases 1 to 25)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathia; Muridae; Mus; 1 (bases 1 to 25)

REFERENCE

Dunn, D., Ayoub, A., Barber, M., Beaton, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, P., Tingley, A., von Niederhausern, A., and Wright, D., Weiss, R.

Dunn, D., Ayoub, A., Barber, M., Beaton, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, P., Tingley, A., von Niederhausern, A., and Wright, D., Weiss, R.

Dunn, D., Ayoub, A., Barber, M., Beaton, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, P., Tingley, A., von Niederhausern, A., and Wright, D., Weiss, R.

Dunn, D., Ayoub, A., Barber, M., Beaton, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, P., Tingley, A., von Niederhausern, A., and Wright, D., Weiss, R.

Dunn, D., Ayoub, A., Barber, M., Beaton, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, P., Tingley, A., von Niederhausern, A., and Wright, D., Weiss, R.

Dunn, D., Ayoub, A., Barber, M., Beaton, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, P., Tingley, A., von Niederhausern, A., and Wright, D., Weiss, R.

Dunn, D., Ayoub, A., Barber, M., Beaton, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, P., Tingley, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

Contact: Robert B. Weiss

Contact: Robert B. Weiss

Contact: Robert B. Weiss

Contact: Robert B. Weiss

Contact: Robert B. Weiss

Contact: Robert B. Weiss

Class: plasmid ends  
High quality sequence stops: 22  
Location/Qualifiers

## FEATURES

1..22  
/organism="Mus musculus"

/strain="C57Bl/6J"

/db\_xref="taxon:10090"

/clone="M06C2M0157C1A"

/clone\_lib="Mouse 10kb plasmid M06C1M library"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, 11-resistant, F<sup>+</sup>"

/note="Vector: pM42nt; purified genomic DNA from M. musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

(http://www.jax.org/resources/c57bl6-antibodies/). The DNA was hydrosulfonically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pM42 (94147321:141491322.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

18 a 0 c 4 d 0 t

## ORIGIN

Query Match 0.48; Score 16; DB 13; Length 22;  
Best Local Similarity 100.0%; Prod. No. 2.5e+04;  
Matches 16; Complement 0; Mismatches 0; Indels 0; Gaps 0;

yy 1797 tttttttttttttttttttt 1812

db 19 tttttttttttttttttttt 4

## RESULT 6

AZ766246

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ766246 2.4 bp DNA GSS 16-FEB-2001  
M0563108R Mouse 10kb plasmid M06C1M library Mus musculus genomic  
clone M0631M0764023 R, DNA sequence  
AZ766246  
GSS:  
AZ766246.1 GI:12884119  
house mouse;  
Mus musculus;  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
1 (bases 1 to 24)  
Dunn, D., Ayoub, A., Barber, M., Beaman, T., Duval, B., Ham, J.,  
Islam, H., Lomax, S., Mahmoud, M., Mowbray, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tracey, A., von Nierhausen, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contract: contract to  
University of Utah Genome Center  
University of Utah  
Rm. 408, Biomedical Polymers Research Bldg., 20 S. 2040 E., Salt, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: adum@genome.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Platform: 0564 row: 1 column: 08

Seq primer: CATACAGGAAACAGCTATGATC  
Class: plasmid ends  
High quality sequence stops: 24  
Location/Qualifiers

## FEATURES

1..23  
/organism="Mus musculus"

/strain="C57Bl/6J"

/db\_xref="taxon:10090"

/clone="M06C1M0563108"

/clone\_lib="Mouse 10kb plasmid M06C1M library"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, 11-resistant, F<sup>+</sup>"

/note="Vector: pM42nt; purified genomic DNA from M. musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

(http://www.jax.org/resources/c57bl6-antibodies/). The DNA was hydrosulfonically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pM42 (94147321:141491322.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

0 a 14 c 0 g 9 t

## ORIGIN

Query Match 0.48; Score 16; DB 13; Length 24;  
Best Local Similarity 100.0%; Prod. No. 2.5e+04;  
Matches 16; Complement 0; Mismatches 0; Indels 0; Gaps 0;

yy 2148 tttttttttttttttttttt 2163

db 1 tttttttttttttttttttt 16

## RESULT 7

T80419

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

T80419 25 bp mRNA EST 15-MAR-1995  
y017411.s1 Soares fetal liver splice UNFS Homo sapiens cDNA clone  
IMAGE:105013 similar to 4b:M42902 PROSTATE ACID PHOSPHATASE  
PRECEDENCE (HUMAN); mRNA sequence.  
T80419  
T80419.1 GI:698928  
EST:  
human;  
Homo sapiens;  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;  
1 (bases 1 to 25)  
Hillier, L., Clark, N., Dubnau, J., Elliston, K., Hawkins, M., Holman,  
M., Hollman, M., Kibara, T., Lee, M., Lamm, G., Marra, M., Parsons, J.,  
Ritkin, L., Rohlfing, T., Soares, M., Tan, F., Tsvetkov, E., Watson,  
R., Williamson, A., Woldman, P., and Wilson, R.  
The WashU-Merck EST project  
Unpublished (1995)  
Contract: y017411.s1  
contact: Wilson RK  
Washington University School of Medicine  
4445 Forest Park Parkway, Box 8001, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Insert Size: 893  
High quality sequence stops: 1 High quality sequence stops: 1





## SOURCE

1. 25  
/organism "Mus musculus"  
/strain "C57BL/6J"  
/db\_xref "taxon:10090"  
/clone "M008011B"  
/vector "pUC19" plasmid library

## BASE COUNT

12 a 7 c 0 g 6 t

## BASE COUNT

6 a 0 c 0 g 22 t

## Query Match

Best Local Similarity 100.0%; Prod. No. 7.6e+04;  
Matches 15; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

## Query Match

Best Local Similarity 100.0%; Prod. No. 7.7e+04;  
Matches 15; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

QY 3073 ttattattattatt 3087  
|||||  
DB 24 ttattattattatt 10

QY 3073 ttattattattatt 3087  
|||||  
DB 2 ttattattattatt 16

## RESULT 10

AZ445640 28 bp DNA GSS 29-SEP-2000  
LOCUS M008012AF Mouse 10kb plasmid M0081M library Mus musculus genomic  
DEFINITION clone U00C1M008012A F. DNA sequence.

AZ428669 28 bp DNA GSS 04-SEP-2000  
LOCUS M0212G1AF Mouse 10kb plasmid M0081M library Mus musculus genomic  
DEFINITION clone U00C1M0212G1A F. DNA sequence.

ACCESSION AZ445640.1 GI:10424877  
VERSION GSS  
KEYWORDS house mouse;  
SOURCE Mus musculus  
ORGANISM Mus musculus

ACCESSION AZ428669  
VERSION GSS  
KEYWORDS house mouse;  
SOURCE Mus musculus  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Dunn, D., Ayoub, A., Barber, M., Beacorn, T., Bival, B., Hamill, C.,  
Islam, H., Jongagere, S., Mahmood, M., Meenen, E., Pedersen, T., Kelly,  
M., Kose, M., Kose, R., Stokes, R., Tinney, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 408, Biomedical Polymers Research Bldg., 20 S. 2030 E., Salt, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0080 row: 1 column: 24  
Seq primer: GCTGTAAACACACGCTACT  
Class: plasmid ends  
High quality sequence stop: 28.

REFERENCE  
AUTHORS Dunn, D., Ayoub, A., Barber, M., Beacorn, T., Bival, B., Hamill, C.,  
Islam, H., Jongagere, S., Mahmood, M., Meenen, E., Pedersen, T., Kelly,  
M., Kose, M., Kose, R., Stokes, R., Tinney, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 408, Biomedical Polymers Research Bldg., 20 S. 2030 E., Salt, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0212 row: 6 column: 14  
Seq primer: GCTGTAAACACACGCTACT  
Class: plasmid ends

## TITLE

## JOURNAL

## COMMENT

## FEAT RES

## SOURCE

## Location/Qualifiers

1. 28  
/organism "Mus musculus"  
/strain "C57BL/6J"  
/db\_xref "taxon:10090"  
/clone "M008011B"  
/vector "pUC19" plasmid library

## BASE COUNT

6 a 0 c 0 g 22 t

## Query Match

Best Local Similarity 100.0%; Prod. No. 7.7e+04;  
Matches 15; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

QY 3073 ttattattattatt 3087  
|||||  
DB 2 ttattattattatt 16

## RESULT 11

AZ428669 28 bp DNA GSS 04-SEP-2000  
LOCUS M0212G1AF Mouse 10kb plasmid M0081M library Mus musculus genomic  
DEFINITION clone U00C1M0212G1A F. DNA sequence.

ACCESSION AZ428669  
VERSION GSS  
KEYWORDS house mouse;  
SOURCE Mus musculus  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Dunn, D., Ayoub, A., Barber, M., Beacorn, T., Bival, B., Hamill, C.,  
Islam, H., Jongagere, S., Mahmood, M., Meenen, E., Pedersen, T., Kelly,  
M., Kose, M., Kose, R., Stokes, R., Tinney, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 408, Biomedical Polymers Research Bldg., 20 S. 2030 E., Salt, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0212 row: 6 column: 14  
Seq primer: GCTGTAAACACACGCTACT  
Class: plasmid ends

## TITLE

## JOURNAL

## COMMENT

FEATURES High quality sequence stop: 28.  
Location/Qualifiers  
1..28

source  
organism="Mus musculus"  
strain="C57BL/6J"  
sex="Male"  
clone="M022M064422"  
vector="pUC19"  
lab\_host="E. coli strain XL10-Gold, TI-resistant, F"  
note="Vector: pM022M064422 was extracted from the Mus musculus C57BL/6J (male) was extracted from the 15 kb laboratory mouse DNA resource.  
(http://www.jax.org/ncic/ncic-clone-center/) The DNA was hydrolyzed and sheared by repeated passage through a 0.005 inch orifice to generate fragments. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pM022 (3117221141bAF12922.1), a copy number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapter mouse DNA was annealed to adaptor vector DNA and transformed into chemically-competent F. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
18 a 5 c 1 g 4 t

Query Match 0.48; Score 15; DB 13; Length 28;  
Best Local Similarity 100.0%; Pred. No. 7.7e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3073 tttattattatta 3087  
DB 27 tttattattatttta 13

RESULT 12  
LOCUS AZ804183 29 bp DNA GSS 15 FEB 2001  
DEFINITION M022M064422 Mouse 10kb plasmid library Mus musculus genomic clone 006C1M062P08 F, DNA sequence.  
ACCESSION AZ804183  
VERSION AZ804183.1 GI:12956506  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Rodentia; Scuriromorphi; Muridae; Murinae; Mus; 1 (bases 1 to 29)  
Dunn, D., Aoyagi, A., Barber, M., Beauchamp, T., Duvall, B., Hamill, J., Islam, H., Loojansse, S., Mahmood, M., Menon, F., Pridmore, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Research Bldg. 20 S. 2000 E. St. UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduan@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0064 Row: N Column: 22  
Seq primer: CAGACGGAACACGCTATTGAC

class: plasmid ends  
High quality sequence stop: 29.  
Location/Qualifiers  
1..29

source  
organism="Mus musculus"  
strain="C57BL/6J"  
sex="Male"  
clone="M022M064422"  
vector="pUC19"  
lab\_host="E. coli strain XL10-Gold, TI-resistant, F"  
note="Vector: pM022M064422 was extracted from the Mus musculus C57BL/6J (male) was extracted from the 15 kb laboratory mouse DNA resource.  
(http://www.jax.org/ncic/ncic-clone-center/) The DNA was hydrolyzed and sheared by repeated passage through a 0.005 inch orifice to generate fragments. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pM022 (3117221141bAF12922.1), a copy number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapter mouse DNA was annealed to adaptor vector DNA and transformed into chemically-competent F. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.48; Score 15; DB 13; Length 29;  
Best Local Similarity 100.0%; Pred. No. 7.7e-04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1039 aaaaagaaagaaa 1054  
DB 14 AFAAGGAGAGAGAA 28

RESULT 13  
LOCUS AZ333223 15 bp DNA GSS 29 SEP 2000  
DEFINITION M022M064422 Mouse 10kb plasmid library Mus musculus genomic clone 006C1M062P08 F, DNA sequence.  
ACCESSION AZ333223  
VERSION AZ333223.1 GI:10497629  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Rodentia; Scuriromorphi; Muridae; Murinae; Mus; 1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beauchamp, T., Duvall, B., Hamill, J., Islam, H., Loojansse, S., Mahmood, M., Menon, F., Pridmore, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Research Bldg. 20 S. 2000 E. St. UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduan@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0062 Row: P Column: 08







adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (314722114[BlA120072.1]), a copy number unstable derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 3 c 2 g 11 t  
ORIGIN

Query Match 0.48; Score 14; DB 13; Length 25;  
Best Local Similarity 100.0%; Pos. No. 2 (0-05);  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3248 atattatcgatt 3261

Db 1 atattatcgatt 14

RESULT 20  
A2840538 25 bp DNA GSS 20-FEB-2001

LOCUS 20146147 Mouse 10kb plasmid U06C1M library Mus musculus genomic  
DEFINITION clone U06C2M0138F10 F, DNA sequence.

ACCESSION A2840538

VERSION A2840538.1 GI:13010446

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
1 (bases 1 to 25)  
Pom, D., Ayagi, A., Barber, M., Beermann, T., Buval, F., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.  
and Wright, P., Weiss, P.

REFERENCE

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0138 row: F column: 10  
Seq primer: CGTTGTAACACGACGCCACAT  
Class: plasmid ends  
High quality sequence stop: 25.

FEATURES  
Location/Qualifiers

1..25  
/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="U06C2M0138F10"

/clone\_lib="Mouse 10kb plasmid U06C1M library"

/sex="Male"

/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector, 10kb, full-length genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/common-features/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (314722114[BlA120072.1]), a copy number  
unstable derivative of plasmid p1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 10 a 0 c 15 g 0 t  
ORIGIN

Query Match 0.49; Score 14; DB 13; Length 25;  
Best Local Similarity 100.0%; Pos. No. 2 (0-05);  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 qdaaagaqaaqaaq 1162

Db 1 GGAGAGAGAGAGAG 14

RESULT 21  
A2416143 27 bp DNA GSS 01-FEB-2000

LOCUS 1M01516147 Mouse 10kb plasmid U06C1M library Mus musculus genomic  
DEFINITION clone U06C1M0191G14 F, DNA sequence.

ACCESSION A2416143

VERSION A2416143.1 GI:10540156

KEYWORDS GSS.

SOURCE house mouse.

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
1 (bases 1 to 27)  
Pom, D., Ayagi, A., Barber, M., Beermann, T., Buval, F., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.  
and Wright, P., Weiss, P.

REFERENCE

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0191 row: G column: 14  
Seq primer: CGTTGTAACACGACGCCACAT  
Class: plasmid ends  
High quality sequence stop: 27

FEATURES  
Location/Qualifiers

1..27  
/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="U06C1M0191G14"

/clone\_lib="Mouse 10kb plasmid U06C1M library"

/sex="Male"

/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector, 10kb, full-length genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/common-features/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end repaired with T4 DNA polymerase and T4





6.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11472114[phAT10972.1]), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

Query Match  
Best local Similarity 100.0%; Prod. No. 2.4e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2146 cctctctctctctc 2159  
|||||  
DB 14 CCTCTCTCTCTCTC 27

RESULT 24  
LOCUS AZ942002 27 bp DNA GSS 26 APR 2002  
DEFINITION 2M052020E3F Mouse 10kb Plasmid U9302M library Mus musculus genomic clone U9302M052020E3 F, DNA sequence.  
ACCESSION AZ942002  
VERSION AZ942002.1 GI:11780498  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Murinae; Mus; 1 (bases 1 to 27)  
AUTHORS Dunn, D., Ayoub, A., Barber, M., Haegele, T., Jural, B., Hamill, C., Islam, H., Londeca, S., Mahmoud, M., Meenen, E., Pedersen, J., Kelly, M., Rose, M., F. von R., Stokes, F., Tinney, A., von Nischelhauser, A., and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert R. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0202 row: B column: 03  
Seq primer: CGTTGTAACACACGGCCACT  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers  
1..27  
/organism="Mus musculus"  
/strain="G57H/4.1"  
/db\_xref="taxon:10090"  
/clone="2M052020E3F"  
/clone\_1kb="Mouse 10kb plasmid U9302M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus G57H/4.1 (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/communityscreens>) The DNA

BASE COUNT  
ORIGIN  
0 a 16 c 0 g 11 t  
Query Match  
Best local Similarity 100.0%; Prod. No. 2.4e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1040 cagatgagatgata 1054  
|||||  
DB 19 GAGATGAGATGATA 6

RESULT 25  
LOCUS AZ656764 28 bp DNA GSS 14 FEB 2000  
DEFINITION 1M052020E5F Mouse 10kb Plasmid U9302M library Mus musculus genomic clone U9302M052020E5 R, DNA sequence.  
ACCESSION AZ656764  
VERSION AZ656764.1 GI:11794910  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Murinae; Mus; 1 (bases 1 to 28)  
AUTHORS Dunn, D., Ayoub, A., Barber, M., Haegele, T., Jural, B., Hamill, C., Islam, H., Londeca, S., Mahmoud, M., Meenen, E., Pedersen, J., Kelly, M., Rose, M., F. von R., Stokes, F., Tinney, A., von Nischelhauser, A., and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert R. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0512 row: F column: 05  
Seq primer: CACATGAGAAACAGCTATATAC  
Class: plasmid ends  
High quality sequence stop: 28.  
Location/Qualifiers  
1..28  
/organism="Mus musculus"  
/strain="G57H/4.1"  
/db\_xref="taxon:10090"  
/clone="1M052020E5F"  
/clone\_1kb="Mouse 10kb plasmid U9302M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus G57H/4.1 (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/communityscreens>) The DNA

#### FEATURES

source  
1..27  
/organism="Mus musculus"  
/strain="G57H/4.1"  
/db\_xref="taxon:10090"  
/clone="2M052020E3F"  
/clone\_1kb="Mouse 10kb plasmid U9302M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus G57H/4.1 (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/communityscreens>) The DNA

source  
1..28  
/organism="Mus musculus"  
/strain="G57H/4.1"  
/db\_xref="taxon:10090"  
/clone="1M052020E5F"  
/clone\_1kb="Mouse 10kb plasmid U9302M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus G57H/4.1 (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/communityscreens>) The DNA



musculus (strain: 661) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/research/subcontractors.htm>). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD12 (4147321143E/AT2972.1), a vector number indicative derivative of pBluescript II. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 11 c 2 g 16 t  
ORIGIN

Query Match 0.4% Score 14 DB 13 Length 29  
Best Local Similarity 100.0% Pred No. 24005  
Matches 14: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1152 aagaaagagagaga 1165  
|||||  
DB 19 AAGAGAGAGAGAGA 6

RESULT 28  
ACCESSION AZ335657 30 bp DNA GSS 29 SEP 2000  
LOCUS M0065016 Mouse 10kb plasmid U00C1M library Mus musculus genomic  
DEFINITION clone U00C1M0065016 R. 1NA sequence.  
ACCESSION AZ335657  
VERSION AZ335657.1 GI:10404189  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus  
1 (bases 1 to 30)  
Dunn, D., Aoyagi, A., Harper, M., Bearson, T., Javal, R., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Petersen, P., Reilly, M., Rose, M., Rose, R., Stevens, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, P.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Published (2000)  
Contact: Robert R. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 N. 2000 E., Salt, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0065 Row: 0 Column: 16  
Seq primer: CACACAGCAAGACACGATATGACG  
Class: Plasmid ends  
High quality sequence stop: 30.  
Location/Qualifiers  
1..30  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U00C1M0065016"  
/clone\_lib="Mouse 10kb plasmid U00C1M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, p-"

FEATURES  
SOURCE

Whole "Vector: pMD12" Purified genomic DNA from M. musculus (strain: 661) (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/research/subcontractors.htm>). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD12 (4147321143E/AT2972.1), a vector number indicative derivative of pBluescript II. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 14 a 4 c 1 g 12 t  
ORIGIN

Query Match 0.4% Score 14 DB 13 Length 30  
Best Local Similarity 100.0% Pred No. 24005  
Matches 14: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 4064 attattattatt 4077  
|||||  
DB 25 ATTATTATTATT 12

RESULT 29  
ACCESSION BC668047 32 bp cDNA EST 30 APR 2001  
LOCUS BC668047  
DEFINITION BC668047 Rat brain library partial cDNA clone BC668047  
ACCESSION BC668047  
VERSION BC668047.1 GI:11889969  
KEYWORDS EST.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
katvus.  
1 (bases 1 to 18)  
Xiao, H., Han, Y., Chang, F., Xu, H., Huang, S., Fan, Y., Li, Bao, L., Peng, L., Gao, C., Yao, Q., Jiang, X., Zhu, Z., Li, X., Li, N., Chen, Z., and Zhang, X.  
Induced gene expression profiles of rat dorsal root ganglion induced by peripheral nerve axotomy  
Published (2001)  
Contact: Zhang Xu  
Laboratory of Sensory System  
Institute of Biotechnology  
420 You Yang Road, Shanghai 200041, P.R.China  
Tel: 86-21-64714870-121  
Fax: 86-21-64714446  
Email: xu.zhang@ion.ac.cn  
This clone is also available at Chinese National Human Genome Center at Shanghai, 453 Guo Sheng Road, Shanghai Hi-Tech Park, Pudong New Area, P. R. China. Please contact with Zhang Xu (xuzhang@ion.ac.cn) or Han Zengnan (hanzengnan@ion.ac.cn) for primers.  
KEYWORDS T3  
PcMWARD: T3  
INCKWARD: T7  
Seq primer: T3  
polyA-No.  
Location/Qualifiers  
1..18  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"

FEATURES  
SOURCE



of pMD42 (q1147221144/AP12002.1), a copy number  
inducible derivative of plasmid p1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The shored, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance.

BASE COUNT  
ORIGIN  
0 a 10 c 0 g 9 t

Query Match  
Best Local Similarity 100.0%; Pred. No. 7, 1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1153 aqagaqagaqaga 1165  
DB 18 AGACAGACAGAGA 6

RESULT 32  
A2510952 19 bp DNA GSS 27 APR 2001  
LOCUS 1M9355615R Mouse 10kb plasmid insert library Mus musculus genomic  
DEFINITION clone JMGCM0355015 R. DNA sequence.  
ACCESSION A2510952  
VERSION A2510952.1 GI:13692208  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Mammalia: Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Ismail, H., Longo, S., Mahmoud, M., Momen, F., Pedersen, J., Kelly,  
M., Rose, M., Rose, F., Stokes, R., Tinney, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Pm. 308, Biomedical Polymers Research Bldg., 20 S. 2000 E., StG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0355 row: G column: 15  
Seq primer: CACACGACGAACAGTATATACG  
Class: plasmid ends  
High quality sequence stop: 19.

#### FEATURES

source  
Location/Qualifiers  
1..19

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="JMGCM0355015"  
/sequence="Mouse 10kb plasmid insert library"  
/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F"  
/note="Vector: pMD42; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/mouse\_dna\_resource/). The DNA  
was hydrolytically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electroporation. Vector RNA was prepared from a derivative  
of pMD42 (q1147221144/AP12002.1), a copy number  
inducible derivative of plasmid p1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The shored, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance.

BASE COUNT  
ORIGIN  
0 a 10 c 0 g 9 t

Query Match  
Best Local Similarity 100.0%; Pred. No. 7, 1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1153 aqagaqagaqaga 1165  
DB 19 AGACAGACAGAGA 7

RESULT 33  
A2983014 19 bp DNA GSS 27 APR 2001  
LOCUS 2M9355615R Mouse 10kb plasmid insert library Mus musculus genomic  
DEFINITION clone JMGCM0355015 R. DNA sequence.  
ACCESSION A2983014  
VERSION A2983014.1 GI:13894241  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Mammalia: Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Ismail, H., Longo, S., Mahmoud, M., Momen, F., Pedersen, J., Kelly,  
M., Rose, M., Rose, F., Stokes, R., Tinney, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Pm. 308, Biomedical Polymers Research Bldg., 20 S. 2000 E., StG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0264 row: H column: 02  
Seq primer: CTTGTAAATACACACACACAT  
Class: plasmid ends  
High quality sequence stop: 19.

#### FEATURES

source  
Location/Qualifiers  
1..19

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="JMGCM0355015"  
/sequence="Mouse 10kb plasmid insert library"  
/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F"  
/note="Vector: pMD42; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/mouse\_dna\_resource/). The DNA  
was hydrolytically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size selected for a 9.5 to

10-5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (q11472114/AF129072.1), a copy number indicator derivative of plasmid p1. The vector was ligated with adaptors complementary to the insect adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT  
0 a 9 c 1 g 9 t

Query Match 0.4% Score 142 DB 142 Length 192  
Post Local Similarity 100.0% Prod. No. 7.1e+055  
Matches 142 Conservative 02 Mismatches 02 Indels 0 Gaps 02

QY 1153 aaaaagagagagaa 1165  
|||||  
DB 19 ACACACACACACAC 7

RESULT 44  
AZ43566/7 20 bp DNA GSS 03 OCT 2000  
LOCUS  
DEFINITION  
1M02196702R Mouse 10kb plasmid 1M02196702R Mus musculus genomic  
clone 1M02196702R. DNA sequence.  
ACCESSION  
AZ43566  
KEYWORDS  
GSS:  
house mouse;  
SOURCE  
Mus musculus  
ORGANISM  
Eukaryota; Metazoa; Chordata; Eumetazoa; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
1 (bases 1 to 20)

REFERENCE  
AUTHORS  
Ismail, H.; Jannat, S.; Mahmood, M.; Mooney, E.; Pederson, J.; Reilly, M.; Rost, M.; Rost, R.; Stokes, R.; Ilany, A.; von Nischkowsky, A. and Wright, D.; Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert R. Weiss  
University of Utah  
Rm. 408, Biomedical Polymers Research Bldg., 20 S. 2030 E., Salt, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@polymers.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate(s): 0219 Row(s) column: 02  
Seq. primer: GATCAGCAACATGACTATATGTC  
Class: plasmid ends  
High quality sequence steps: 20

FEATURES  
SOURCE  
1..20  
Location/Qualifiers

/organism "Mus musculus"  
/strain "G11472114/AF129072.1"  
/clone "1M02196702R"  
/sex "Male"  
/lab host "E. coli strain XL10-Gold, II resistant, F"  
/note "Vector: 1M02196702R Purified genomic DNA from M.  
musculus c776/7c (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/laboratory-mouse-dna-resource/). The DNA  
was hydrolyzed by sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end repaired with T4 DNA polymerase and T4  
polyphosphatase. Adapted oligonucleotides were  
ligated to the blunt ends in both vector clones. The

adapted DNA was purified and size selected for a 9-9 to 10-5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (q11472114/AF129072.1), a copy number indicator derivative of plasmid p1. The vector was ligated with adaptors complementary to the insect adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT  
0 a 10 c 0 g 10 t

Query Match 0.4% Score 142 DB 142 Length 202  
Post Local Similarity 100.0% Prod. No. 7.1e+055  
Matches 142 Conservative 02 Mismatches 02 Indels 0 Gaps 02

QY 1153 aaaaagagagagaa 1165  
|||||  
DB 20 ACACACACACACAC 8

RESULT 45  
AZ492997/7 20 bp DNA GSS 05 OCT 2000  
LOCUS  
DEFINITION  
1M02278240R Mouse 10kb plasmid 1M02278240R Mus musculus genomic  
clone 1M02278240R. DNA sequence.  
ACCESSION  
AZ492997  
KEYWORDS  
GSS:  
house mouse;  
SOURCE  
Mus musculus  
ORGANISM  
Eukaryota; Metazoa; Chordata; Eumetazoa; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
1 (bases 1 to 20)

REFERENCE  
AUTHORS  
Ismail, H.; Jannat, S.; Mahmood, M.; Mooney, E.; Pederson, J.; Reilly, M.; Rost, M.; Rost, R.; Stokes, R.; Ilany, A.; von Nischkowsky, A. and Wright, D.; Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert R. Weiss  
University of Utah  
Rm. 408, Biomedical Polymers Research Bldg., 20 S. 2030 E., Salt, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@polymers.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate(s): 0427 Row(s) column: 24  
Seq. primer: GATTGTAACATGACATGATGTC  
Class: plasmid ends  
High quality sequence steps: 20

FEATURES  
SOURCE  
1..20  
Location/Qualifiers

/organism "Mus musculus"  
/strain "G11472114/AF129072.1"  
/clone "1M02278240R"  
/sex "Male"  
/lab host "E. coli strain XL10-Gold, II resistant, F"  
/note "Vector: 1M02278240R Purified genomic DNA from M.  
musculus c57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/laboratory-mouse-dna-resource/). The DNA  
was hydrolyzed by sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end repaired with T4 DNA polymerase and T4  
polyphosphatase. Adapted oligonucleotides were  
ligated to the blunt ends in both vector clones. The



[illegible][illegible]



was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 14 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (31473.1141b/AB22072.1), a copy number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10 Gold (Stratagene) cells and selected for ampicillin resistance.

# BASE COUNT

4 a 12 c 0 g 5 t

# ORIGIN

## Query Match

Best Local Similarity 100.0% Prod. No. 7.10-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2155 cctccctccctc 2167  
|||||

DB 7 cctccctccctc 19

## RESULT 40

AZ394897

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

Plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

801 585 5606

84112, USA

tel: 801 585 5606

fax: 801 585 7177

email: ddunne@genetics.utah.edu

Insert length: 10000

Std Error: 0.00

Plate: 0158

row: H column: 11  
Seq primer: CACACAGGAACACCTATGACCT  
Class: plasmid ends  
High quality sequence slope: 21  
location/Qualifiers  
1..21  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="M0043819"  
/clone\_lib="Mouse 10kb plasmid M0043819 library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F"  
/note="Vector: pMD2002; purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse Research Center"

# BASE COUNT

0 a 10 c 0 g 11 t

# ORIGIN

## Query Match

Best Local Similarity 100.0% Prod. No. 7.10-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1154 aagagagagagag 1165  
|||||

DB 21 AGAGAGAGAGAG 9

## RESULT 41

AZ504574

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

Plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

801 585 5606

84112, USA

tel: 801 585 5606

fax: 801 585 7177

email: ddunne@genetics.utah.edu

Insert length: 10000

Std Error: 0.00

Plate: 0043

row: H column: 19  
Seq primer: CATTGTAAGAAATAGGATGAT  
Class: plasmid ends  
High quality sequence slope: 21  
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Matches 11	Conservative	07	Mismatches	07
			Indels	07
			Changes	07
QY 1153	aaagagagagagag	1165		
db 21	AGAGAGAGAGAGA	9		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Classes 1 to 21)	Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.			
Dunn, D., Agya, A., Barber, M., Beacorn, T., Duvai, B., Hamill, J., Islam, H., Longacre, S., Mahmoud, M., Meenon, E., Petersen, J., Kelly, J. M., Rose, P., Rose, P., Stokes, P., Tunoy, A., von Niederhausern, A. and Wright, D., Weiss, R.		Mouse whole genome scaffolding with paired end reads from 10Kb Plasmid Inserts	Unpublished (2000)	Contact: Robert B. Weiss

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FEATURES
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/organism "Mus musculus"
/strain="0557M/61"
/db_xref="d. 11004"
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[illegible]

**JOURNAL** Journal of Cellular Biochemistry  
**EXPERIMENT** Molecular Biology and Cell  
**TITLE** Identification of Expressed Sequence Tags of Schistosoma haematophylos  
**AUTHORS** McElroy M and Mila K.  
**REFERENCE** 1. (Pages 1 to 22)  
**PUBLISHED** Unpublished (1998)  
**CONTACT** Dr. Mila K. McElroy  
Genome Research Group

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Mon Apr 22 08:35:21 2002

us-09-824-322b-1.rst

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Job time: 6879 sec





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1 Sequence: 4. Application US/08434503
2 Patent No. 5616490
3
4 GENERAL INFORMATION:
5 APPLICANT: Sean M. Sullivan
6 APPLICANT: Kenneth G. Draper
7 TITLE OF INVENTION: METHOD AND REAGENT FOR
8 TITLE OF INVENTION: TREATMENT OF INFLAMMATORY
9 TITLE OF INVENTION: DISEASE
10 NUMBER OF SEQUENCES: 54
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Lyon & Lyon
13 STREET: 611 West Sixth Street
14 CITY: Los Angeles
15 STATE: California
16 COUNTRY: USA
17 ZIP: 90017
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
21 COMPUTER: IBM compatible
22 OPERATING SYSTEM: IBM MS DOS (Version 5.0)
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24 SOFTWARE: Wordperfect (Version 5.1)
25
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: US/08/434,503
28 FILING DATE: 04-MAY-1995
29 CLASSIFICATION: 435
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31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 08/008,895
33 FILING DATE: 19-JAN-1993
34 APPLICATION NUMBER: 07/989,849
35 FILING DATE: December 7, 1992
36
37 ATTORNEY/AGENT INFORMATION:
38 NAME: Warburg, Richard J.
39 REGISTRATION NUMBER: 32,327
40 REFERENCE/CKET NUMBER: 295,276
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42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: (213) 489-1600
44 TELEFAX: (213) 955-0440
45
46 TELEX: 67-3510
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48 INFORMATION FOR SEQ ID NO: 4:
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50 SEQUENCE CHARACTERISTICS:
51 LENGTH: 28
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[illegible]

## RESULT 9

PCT US94 10957 10/6  
Sequence 10, Application W/7059410957

## GENERAL INFORMATION:

APPLICANT: Goldstein, Harriet; Kollmann, Tobias R.  
TITLE OF INVENTION: Immunodeficient Mouse Models of  
TITLE OF INVENTION: Pathogenesis of Human Disease and Efficacy and Toxicity of  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESS: Law Office of Sherman and Shalloway  
STREET: 403 N. Washington Street  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 460 kb storage  
COMPUTER: IBM clone, 8088 Turbo  
OPERATING SYSTEM: MS-DOS 5.0  
SOFTWARE: Word Perfect, Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10957  
FILING DATE:

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Richard A. Strohbehn  
REGISTRATION NUMBER: 26,588  
REFERENCE/EXCISE NUMBER: 100-144/511-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 549-2282  
TELEFAX: (703) 846-0106  
INFORMATION FOR SEQ. ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 27 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYDROPHOBIC: no  
ORIGINAL SOURCE:  
ORGANISM: human  
FEATURE:

NAME/KEY: 4' TNE-  
PCT US94 10957 10

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Best Local Similarity 100.0%; Pct. No. 0.008;  
Matches 27; Consensus 0; Mismatches 0; Indels 0; Gaps 0;

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|||||

DB 27 accagatcagatcctcctacacac 1

## RESULT 10

US 08 444 503 17

Sequence 17, Application US/08444503  
Patent No. 5616490

## GENERAL INFORMATION:

APPLICANT: Kenneth G. Diaper  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: TREATMENT OF INFLAMMATORY  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles

STATE: California  
COUNTRY: USA  
ZIP: 90017

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444 503  
FILING DATE: 04 MAY 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/2908,895  
FILING DATE: 19 JAN 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

## ATTORNEY/AGENT INFORMATION:

NAME: Mulbury, Richard J.  
REGISTRATION NUMBER: 42,427  
REFERENCE/EXCISE NUMBER: 200/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
FILING DATE:

## SEQUENCE CHARACTERISTICS:

LENGTH: 26  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-434-503-17

## Query Match

Best Local Similarity 84.6%; Score 26; 106 %; Length 26;  
Matches 22; Consensus 4; Mismatches 0; Indels 0; Gaps 0;

QY 2462 cccatcagatcctcctacacacac 2407  
|||||

DB 1 cccatcagatcctcctacacacac 26

## RESULT 11

US 08 434 503 25

Sequence 25, Application US/08444503  
Patent No. 5616490

## GENERAL INFORMATION:

APPLICANT: Kenneth G. Diaper  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: TREATMENT OF INFLAMMATORY  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444 503  
FILING DATE: 04 MAY 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,895  
FILING DATE: 19 JAN 1993



APPLICATION NUMBER: 07/664,949  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 200/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
FILER: 67-3510  
INFORMATION FOR SEQ. ID NO. 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-434-503-25

Query Match: 0.78; Score 26; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 21; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2897 cagcagatgctgcaatgagc 2922  
DB 1 nccctacaaacccgcagacacacacac 26

RESULT 12  
US-09-176-862-2/8  
Sequence 2: Applicant: us-09-176-862-2  
Patent No. 6046319  
GENERAL INFORMATION:  
APPLICANT: Howey, Christopher  
APPLICANT: Mayne, Michael B.  
TITLE OF INVENTION: ANTISENSE OF DEOXYXYNUCLEOTIDES SPECIFICALLY EXPRESSION  
FILE REFERENCE: 3045.00002  
CURRENT APPLICATION NUMBER: US-09-176-862H  
CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: 60/062,718  
EARLIER FILING DATE: 1997-10-22  
NUMBER OF SEQ. ID NOS: 33  
SOFTWARE: Patent In Ver. 2.0  
SEQ. ID NO. 2  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-176-862-2

Query Match: 0.78; Score 26; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 873 ctccagcagatgctgcttctccagc 898  
DB 26 cttctacaaacccgcagacacacacac 1

RESULT 13  
US-09-176-862-9/6  
Sequence 9: Applicant: us-09-176-862-9  
Patent No. 6046319  
GENERAL INFORMATION:  
APPLICANT: Howey, Christopher  
APPLICANT: Mayne, Michael B.  
TITLE OF INVENTION: ANTISENSE OF DEOXYXYNUCLEOTIDES SPECIFICALLY EXPRESSION  
FILE REFERENCE: 3045.00002  
CURRENT APPLICATION NUMBER: US-09-176-862H

CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: 60/062,718  
EARLIER FILING DATE: 1997-10-22  
NUMBER OF SEQ. ID NOS: 33  
SOFTWARE: Patent In Ver. 2.0  
SEQ. ID NO. 9  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-176-862-9

Query Match: 0.78; Score 26; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2216 ccaagcagcctcctgagcagatgctg 2241  
DB 26 ctaattccctcctgagcagatgctg 1

RESULT 14  
US-09-176-862-11/6  
Sequence 11: Applicant: us-09-176-862-11  
Patent No. 6046319  
GENERAL INFORMATION:  
APPLICANT: Howey, Christopher  
APPLICANT: Mayne, Michael B.  
TITLE OF INVENTION: ANTISENSE OF DEOXYXYNUCLEOTIDES SPECIFICALLY EXPRESSION  
FILE REFERENCE: 3045.00002  
CURRENT APPLICATION NUMBER: US-09-176-862H  
CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: 60/062,718  
EARLIER FILING DATE: 1997-10-22  
NUMBER OF SEQ. ID NOS: 33  
SOFTWARE: Patent In Ver. 2.0  
SEQ. ID NO. 11  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-176-862-11

Query Match: 0.78; Score 26; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 aagcagcagcctcctgagcagatgctg 860  
DB 26 ctaattccctcctgagcagatgctg 1

RESULT 15  
US-09-176-862-12/6  
Sequence 12: Applicant: us-09-176-862-12  
Patent No. 6046319  
GENERAL INFORMATION:  
APPLICANT: Howey, Christopher  
APPLICANT: Mayne, Michael B.  
TITLE OF INVENTION: ANTISENSE OF DEOXYXYNUCLEOTIDES SPECIFICALLY EXPRESSION  
FILE REFERENCE: 3045.00002  
CURRENT APPLICATION NUMBER: US-09-176-862H  
CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: 60/062,718  
EARLIER FILING DATE: 1997-10-22  
NUMBER OF SEQ. ID NOS: 33  
SOFTWARE: Patent In Ver. 2.0

```

1 SEQ ID NO 12
2 LENGTH: 26
3 TYPE: DNA
4 ORGANISM: Artificial Sequence
5 FEATURE:
6 OTHER INFORMATION: Description of Artificial Sequence:synthetic
US 09 176 862 12

```

```

Query Match          0.78; Score 26; DB 4; Length 26;
Post Local Similarity 100.0%; Prod. No. 0.0243
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 845 1cccccaaaagcagagagagagagag 870
DB 26 1cccccaaaagcagagagagagagag 1

```

```

RESULT 16
US 09 176 862 142
1 Sequence 15, Application US/09176862B
2 Patent No. 6046319
3 GENERAL INFORMATION:
4 APPLICANT: Innot, Christopher
5 APPLICANT: Innot, Michael R.
6 TITLE OF INVENTION: ANTISENSE OF PROTEIN SYNTHETIC DEGRADATION EXPERTISE
7 FILE REFERENCE: 6045,00002
8 CURRENT APPLICATION NUMBER: 09/09176,862B
9 CURRENT FILING DATE: 1999 10 22
10 EARLIER APPLICATION NUMBER: 60/062,718
11 EARLIER FILING DATE: 1997 10 22
12 NUMBER OF SEQ ID NOS: 34
13 SOFTWARE: Patent In Ver. 2.0
14 SEQ ID NO 15
15 LENGTH: 26
16 TYPE: DNA
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Description of Artificial Sequence:synthetic
US 09 176 862 14

```

```

Query Match          0.78; Score 26; DB 4; Length 26;
Post Local Similarity 100.0%; Prod. No. 0.0243
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 855 4cccccaaaagcagagagagagagag 880
DB 26 4cccccaaaagcagagagagagagag 1

```

```

RESULT 17
US 09 149 922 55
1 Sequence 55, Application US/09149922A
2 Patent No. 6256174
3 GENERAL INFORMATION:
4 APPLICANT: Innot, Robert
5 APPLICANT: Innot, Robert
6 APPLICANT: Innot, William R.
7 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING AND MODULATING
8 TITLE OF INVENTION: PROTEIN PROTEIN INTERACTIONS
9 FILE REFERENCE: 9366,006
10 CURRENT APPLICATION NUMBER: 09/09149,922A
11 CURRENT FILING DATE: 1999 09 09
12 EARLIER APPLICATION NUMBER: 60/064,058
13 EARLIER FILING DATE: 1997 11 04
14 NUMBER OF SEQ ID NOS: 97
15 SOFTWARE: Patent In Ver. 2.0
16 SEQ ID NO 55
17 LENGTH: 26
18 TYPE: DNA
19 ORGANISM: Artificial Sequence

```

```

1 FEATURE:
2 OTHER INFORMATION: Description of Artificial Sequence: primer
US 09 149 922 55

```

```

Query Match          0.78; Score 26; DB 4; Length 26;
Post Local Similarity 100.0%; Prod. No. 0.0243
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 776 1cccccaaaagcagagagagagagag 801
DB 1 1cccccaaaagcagagagagagagag 26

```

```

RESULT 18
US 09 166 186 45
1 Sequence 45, Application US/09166186A
2 Patent No. 6080580
3 GENERAL INFORMATION:
4 APPLICANT: Baker, Brenda
5 APPLICANT: Baker, Brenda
6 APPLICANT: Baker, Frank
7 APPLICANT: Baker, Madeline M.
8 APPLICANT: Shandhan, William R.
9 TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES MODULATION OF THE
10 FILE REFERENCE: 1509,0422
11 CURRENT APPLICATION NUMBER: 09/09166,186A
12 CURRENT FILING DATE: 1998 10 05
13 NUMBER OF SEQ ID NOS: 250
14 SEQ ID NO 45
15 LENGTH: 25
16 TYPE: DNA
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: PCR probe
US 09 166 186 45

```

```

Query Match          0.78; Score 25; DB 4; Length 25;
Post Local Similarity 100.0%; Prod. No. 0.0643
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 900 cttctctctctctctctctctctctct 924
DB 1 cttctctctctctctctctctctctct 25

```

```

RESULT 19
US 09 313 942 45
1 Sequence 45, Application US/09313942A
2 Patent No. 6228642
3 GENERAL INFORMATION:
4 APPLICANT: Baker, Brenda
5 APPLICANT: Baker, Frank
6 APPLICANT: Baker, Madeline M.
7 APPLICANT: Shandhan, William R.
8 TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES MODULATION OF THE
9 FILE REFERENCE: 1509,0456
10 CURRENT APPLICATION NUMBER: 09/09313,942A
11 CURRENT FILING DATE: 1999 05 18
12 NUMBER OF SEQ ID NOS: 501
13 SEQ ID NO 45
14 LENGTH: 25
15 TYPE: DNA
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: PCR probe
US 09 313 942 45

```

```

Query Match          0.78; Score 25; DB 4; Length 25;
Post Local Similarity 100.0%; Prod. No. 0.0643
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



COUNTRY: U.S.A.  
 ZIPT: 77010 4095  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISK, 3.5 inch (1.44MB)  
 COMPUTER: IBM PC/AT  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: BASIC  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-07/647,655C  
 FILING DATE: 19910131  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: THOMAS D. PAUL  
 REGISTRATION NUMBER: 32,714  
 REFERENCE/BOOKET NUMBER: D-5217  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (713) 651-5246  
 TELEFAX: (713) 651-5246  
 TELEX: WESTERN UNION 762429  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Genomic DNA  
 US-07-647-655C-15

Query Match 0.78; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Prod. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1171 gaaagacagatctctgagatc 1194  
 |||||||  
 DB 1 gcaatcagcagatctctgagatc 24

RESULT 24  
 US-07-647-655C-16/C  
 Sequence 16, Application US/07647655C  
 Patent No. 5,464,759  
 GENERAL INFORMATION:  
 APPLICANT: Albert O. Edwards and  
 APPLICANT: Charles Thomas Caskey  
 TITLE OF INVENTION: DNA profiling with short  
 TITLE OF INVENTION: tandem repeat polymorph. Isms and identification of polymorphic  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Pulidotti & Jaworski, Patent Department  
 STREET: 1401 McKinney, Suite 5100  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: U.S.A.  
 ZIPT: 77010 4095  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISK, 3.5 inch (1.44MB)  
 COMPUTER: IBM PC/AT  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: BASIC  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-07/647,655C  
 FILING DATE: 19910131  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: THOMAS D. PAUL

REGISTRATION NUMBER: 32,714  
 REFERENCE/BOOKET NUMBER: D-5217  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (713) 651-5246  
 TELEFAX: (713) 651-5246  
 TELEX: WESTERN UNION 762429  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Genomic DNA  
 US-07-647-655C-16

Query Match 0.78; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Prod. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1456 tatagacgagagagagatg 1479  
 |||||||  
 DB 24 tatagacgagagagagatg 1

RESULT 25  
 US-08-434-503-4  
 Sequence 4, Application US/08434503  
 Patent No. 5616490  
 GENERAL INFORMATION:  
 APPLICANT: Scott M. Sullivan  
 APPLICANT: Kenneth G. Draper  
 TITLE OF INVENTION: METHOD AND REAGENT FOR  
 TITLE OF INVENTION: TREATMENT OF INFLAMMATORY  
 TITLE OF INVENTION: DISEASE  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Lyon & Lyon  
 STREET: 611 West Sixth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIPT: 90017  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)  
 SOFTWARE: Wordperfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-08/434,503  
 FILING DATE: 04-MAY-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US-08/008,895  
 FILING DATE: 19-JAN-1994  
 APPLICATION NUMBER: 07/989,849  
 FILING DATE: December 7, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Waldorf, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/BOOKET NUMBER: 259/276  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-4510  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 US-08-434-503-4

Query Match 0.78; Score 24; DB 1; Length 24;  
 Best Local Similarity 91.74; Pred. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 cccctgaacacacccctgaacgc 708  
 |||||  
 DB 1 cccctgaacacacccctgaacgc 24

## RESULT 26

US-08-732-398-4/c  
 Sequence 4; Application US/08732398

Patent No. 5980911  
 GENERAL INFORMATION:

APPLICANT: Corner, Leigh A.  
 APPLICANT: Rothel, James S.

APPLICANT: Seow, Heng F.  
 APPLICANT: Wood, Paul R.

APPLICANT: McWaters, Peter  
 TITLE OF INVENTION: AN ADJUVANT

NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSEP  
 STREET: 400 Garden City Plaza

CITY: Garden City  
 STATE: New York

COUNTRY: United States  
 ZIP: 11530

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/732,398  
 FILING DATE: 11-FEB-1997

CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:

NAME: Disiglio, Frank S.  
 REGISTRATION NUMBER: 31,346

REFERENCE/WORK NUMBER: 10366  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343  
 TELEFAX: (516) 742-4366

TELEX: 230 901 SANS "P"  
 INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs

TYPE: nucleic acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)

US-08-732-398-4

Query Match 0.78; Score 24; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2569 tactttggatcattgcctatga 2592  
 |||||  
 DB 24 tactttggatcattgcctatga 1

## RESULT 27

US-08-859-998-45  
 Sequence 45; Application US/08859998

Patent No. 5994076  
 GENERAL INFORMATION:

APPLICANT: Chenchik, Alex  
 APPLICANT: Johndaze, George

APPLICANT: Bililashvili, Robert

TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
 MEMBER OF INVENTION: EXPRESSION  
 NUMBER OF SEQUENCES: 1375  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.  
 STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park  
 STATE: CA

COUNTRY: US  
 ZIP: 94025

COMPUTER READABLE FORM:  
 MEDIUM TYPE: diskette

COMPUTER: IBM compatible  
 OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/859,998  
 FILING DATE: 21-MAY-1997

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Field, Bret E.

REGISTRATION NUMBER: 37,620  
 REFERENCE/WORK NUMBER: 59,966,702,001

TELEPHONE: 415-422-5070  
 TELEFAX: 415-854-0875

TELECOMMUNICATION INFORMATION:  
 INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs

TYPE: nucleic acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: DNA

FEATURE:  
 OTHER INFORMATION: oligonucleotide primer

US-08-859-998-45

Query Match 0.78; Score 24; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2345 tactttggatcattgcctatga 2368  
 |||||  
 DB 1 tactttggatcattgcctatga 24

## RESULT 28

US-08-859-998-46/c  
 Sequence 46; Application US/08859998

Patent No. 5994076  
 GENERAL INFORMATION:

APPLICANT: Chenchik, Alex  
 APPLICANT: Johndaze, George

APPLICANT: Bililashvili, Robert  
 TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

NUMBER OF SEQUENCES: 1375  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.  
 STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park  
 STATE: CA

COUNTRY: US  
 ZIP: 94025

COMPUTER READABLE FORM:  
 MEDIUM TYPE: diskette

COMPUTER: IBM compatible  
 OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

RESULT 40  
US 09/176,862 15/c  
Sequence 15, Application US/09176862P  
Patent No. 6046319

RESULT: 32  
 US-09-176,862-28/0  
 Sequence 28 Application US/09176862H  
 Patent No. 6,046,819  
 GENERAL INFORMATION:  
 APPLICANT: Power, Christopher  
 APPLICANT: Mayo, Michael H.  
 TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES RESULTING EXPRESSION  
 TITLE OF INVENTION: OF THE ALPHA

FILE REFERENCE: 3045.00002  
CURRENT APPLICATION NUMBER: US/09/176, 86376  
CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: 60/062,718  
EARLIER FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO: 28  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence synthon to  
US-09-176-862-28

Query Match 0.7% Score 24; DB 3; Length 24;  
Best Local Similarity 100.0%; Pctd. No. 0.18;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1612 caagctctagccagatctatd 1625  
DB 24 CAGCTCTAGCCAGATCTATD 1

RESULT 33  
US-08-434-503-9  
Sequence 9, Application US/08434503  
Patent No. 5616490  
GENERAL INFORMATION:  
APPLICANT: Sean M. Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: TREATMENT OF INFLAMMATORY  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,503  
FILING DATE: 04-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,895  
FILING DATE: 19-JAN-1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Walburg, Richard J.  
REGISTRATION NUMBER: 32,827  
REFERENCE/APP. NUMBER: 209,276  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 656-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-434-503-9

Query Match 0.6% Score 24; DB 1; Length 24;  
Best Local Similarity 60.0%; Pctd. No. 0.22  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 881 agatctatccacatctctc 904  
DB 1 GAGTCTATCCACATCTCTC 23

RESULT 34  
PCT-US96-09511 10/c  
Sequence 19, Application PCT/US9609511  
GIBPAT. 19960411 08;  
APPLICANT: Boord, David  
APPLICANT: Eisenlohr, Lawrence and  
APPLICANT: Lalline, Edmund  
TITLE OF INVENTION: COMPOSITION COMPRISING A TUMOR CELL EXTRACT  
TITLE OF INVENTION: AND METHOD OF USING THE COMPOSITION  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. & A. L. WARD, JR. & ASSOCIATES, P.C.  
ADDRESSER: NORRIS  
STREET: One Liberty Place - 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09511  
FILING DATE: June 7, 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/203,004  
FILING DATE: February 28, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: LOFT Y. BOARDOLL  
REGISTRATION NUMBER: 34,293  
REFERENCE/APP. NUMBER: 179,156  
TELEPHONE: (215) 568-8100  
TELEFAX: (215) 568-4439  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MEDIUM TYPE: nucleic acids  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US96-09511-10

Query Match 0.6% Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pctd. No. 0.52  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2579 accttcttcttcttcttcttctt 2592  
DB 23 ACCTTCTTCTTCTTCTTCTTCTT 1

RESULT 35  
US-09-176-862-14/c  
Sequence 14, Application US/0917662B  
Patent No. 6046419  
GENERAL INFORMATION:

1 APPLICANT: Fower, Christopher  
 2 APPLICANT: Mayo, Michael R.  
 3 TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES REGULATING EXPRESSION  
 4 TITLE OF INVENTION: OF THE ALPHA  
 5 FILE REFERENCE: 1041,00002  
 6 CURRENT APPLICATION NUMBER: US/09/176,302B  
 7 EARLIER FILING DATE: 1998-10-22  
 8 EARLIER APPLICATION NUMBER: 60/006,271H  
 9 NUMBER OF FILING DATE: 1997-10-22  
 10 NUMBER OF SEQ ID NOS: 34  
 11 SOFTWARE: Patent In Ver. 2.0  
 12 SEQ ID NO: 14  
 13 LENGTH: 26  
 14 TYPE: DNA  
 15 ORGANISM: Artificial Sequence  
 16 FEATURE:  
 17 OTHER INFORMATION: Description of Artificial Sequence: synbio  
 18 US 09 176-862 14

Query Match 0.68; Score 23; DB 3; Length 26;  
 Best Local Similarity 100.0%; Prod. No. 0.51;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 09 865 cccagagctccagggagctt 887  
 10 26 cccagagctccagggagctt 4

RESULT 36  
 08 07 794 400-24  
 1 Sequence 24, Application US/07/94400  
 2 Patent No. 5422104  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Favors, W.  
 5 APPLICANT: Van Ostad, X.  
 6 TITLE OF INVENTION: TNF-MUTINS  
 7 NUMBER OF SEQUENCES: 24  
 8 CORRESPONDENCE ADDRESS:  
 9 ADDRESSEE: Hoffmann-La Roche Inc.  
 10 STREET: 440 Kingsland Street  
 11 CITY: Nutley  
 12 STATE: New Jersey  
 13 COUNTRY: USA  
 14 ZIP: 07110  
 15 COMPUTER READABLE FORM:  
 16 MEDIUM TYPE: Floppy disk  
 17 OPERATING SYSTEM: pc-jos/ms-dos  
 18 SOFTWARE: Patent In Release #1.0, Version #1.25  
 19 CURRENT APPLICATION DATA:  
 20 APPLICATION NUMBER: US/97/794,400  
 21 FILING DATE: 1997-11-20  
 22 CLASSIFICATION: 435  
 23 PRIOR APPLICATION DATA:  
 24 APPLICATION NUMBER: EP 90810901.0  
 25 FILING DATE: 21 Nov 1990  
 26 ATTORNEY/AGENT INFORMATION:  
 27 NAME: Krowalio, William  
 28 REGISTRATION NUMBER: 44256  
 29 REFERENCE/AGENT NUMBER: 4105/196-00  
 30 TELECOMMUNICATION INFORMATION:  
 31 TELEPHONE: (201) 245-4487  
 32 TELEFAX: (201) 245-4500  
 33 INFORMATION FOR SEQ ID NO: 24:  
 34 SEQUENCE CHARACTERISTICS:  
 35 LENGTH: 22 base pairs  
 36 TYPE: NUCLEIC ACID  
 37 STRANDEDNESS: single  
 38 MOLECULE TYPE: linear  
 39 FEATURE:  
 40

1 NAME/KEY: misc feature  
 2 LOCATION: 1..22  
 3 OTHER INFORMATION: /function "poly primer"  
 4 OTHER INFORMATION: /note "poly primer used in conjunction with Seq.  
 5 OTHER INFORMATION: /note "poly primer used in conjunction with Seq.  
 6 OTHER INFORMATION: ID No. 5422104 22 & 28 to create mutations of TNF alpha  
 7 US-07 794 400-24

Query Match 0.68; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Prod. No. 1.5;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 09 2221 cccagagctccagggagctt 2242  
 10 1 cccagagctccagggagctt 22

RESULT 37  
 US-08-041-648-14  
 1 Sequence 14, Application US/08041648  
 2 Patent No. 5486461  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Lessner, Werner  
 5 APPLICANT: Lischer, Hansruedi  
 6 APPLICANT: St. Ber, Dietrich  
 7 TITLE OF INVENTION: TNF-MUTINS  
 8 NUMBER OF SEQUENCES: 17  
 9 CORRESPONDENCE ADDRESS:  
 10 ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.  
 11 STREET: 440 Kingsland Street  
 12 CITY: Nutley  
 13 STATE: New Jersey  
 14 COUNTRY: U.S.A.  
 15 ZIP: 07110-1199  
 16 COMPUTER READABLE FORM:  
 17 MEDIUM TYPE: Floppy disk  
 18 OPERATING SYSTEM: pc-jos/ms-dos  
 19 SOFTWARE: Patent In Release #1.0, Version #1.25  
 20 CURRENT APPLICATION DATA:  
 21 APPLICATION NUMBER: US/08/041,648  
 22 FILING DATE: 14-8-1993  
 23 CLASSIFICATION: 435  
 24 PRIOR APPLICATION DATA:  
 25 APPLICATION NUMBER: EP 92810249.0  
 26 FILING DATE: 2-APR-1992  
 27 ATTORNEY/AGENT INFORMATION:  
 28 NAME: Possmato, Catherine R.  
 29 REGISTRATION NUMBER: 44240  
 30 REFERENCE/AGENT NUMBER: 44240  
 31 TELECOMMUNICATION INFORMATION:  
 32 TELEPHONE: (201) 245-6208  
 33 TELEFAX: (201) 245-4500  
 34 INFORMATION FOR SEQ ID NO: 14:  
 35 SEQUENCE CHARACTERISTICS:  
 36 LENGTH: 22 base pairs  
 37 TYPE: nucleic acid  
 38 STRANDEDNESS: single  
 39 MOLECULE TYPE: linear  
 40 MOLECULE TYPE: DNA (genomic)  
 41 HYPOHETICAL: NO  
 42 ANTI-SENSE: NO  
 43 ORIGINAL SOURCE:  
 44 ORGANISM: Homo sapiens  
 45 US-08-041-648-14

Query Match 0.68; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Prod. No. 1.5;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 09 2221 cccagagctccagggagctt 2242



Db 1 GGGCTGCTGGCCATGCGGTG6 22

# RESULT 38

US-08-217-529-6  
Sequence 6, Application US/08217529

## GENERAL INFORMATION:

APPLICANT: Hammer, David  
APPLICANT: Lesslauer, Werner  
APPLICANT: Lotscher, Hansruedi  
APPLICANT: Stuber, Dietrich  
TITLE OF INVENTION: Tumor Necrosis Factor Mutations  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSER: George M. Gould, Esq., Holtmann-Ja Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.  
ZIP: 07110

## COMPUTER READABLE FORM:

MEDIUM TYPE: FILE, List  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: pc-pos/ms-dos  
SOFTWARE: Patonin Release #1 9, Version #1 25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/217,529

FILING DATE: 24 MAR 1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93810224.1

FILING DATE: 29-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Roseman, Catherine R

REGISTRATION NUMBER: 34240

REFERENCE/DOCKET NUMBER: 4105/155

TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 235-6208

TELEFAX: (201) 235-6508

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: primate 29, Mpc2

US-08-217-529-6

Query Match 0.58, Score 22, DB 1, Length 22

Best Local Similarity 100.0%; Prod. No. 1.5;

Matches 22; Conservative 0; Mismatches 0; Indels 0;

Gap 0; Cuts 0;

US-08-434-503-15

Sequence 15, Application US/0844503

GENERAL INFORMATION:

APPLICANT: Sean M. Sullivan

APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: METHOD AND REAGENT FOR

TREATMENT OF INFLAMMATORY

TITLE OF INVENTION: DISEASE

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/434,503

FILING DATE: 04-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/008,895

FILING DATE: 19-JAN-1993

APPLICATION NUMBER: 07/989,849

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 42,327

REFERENCE/DOCKET NUMBER: 2062/206

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 449-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 22

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-434-503-15

# RESULT 40

US-08-434-503-28

Sequence 28, Application US/0844503

GENERAL INFORMATION:

APPLICANT: Sean M. Sullivan

APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: METHOD AND REAGENT FOR

TREATMENT OF INFLAMMATORY

TITLE OF INVENTION: DISEASE

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

```

1 APPLICATION NUMBER: US/98/414,503
2 FILING DATE: 04 MAY 1995
3 CLASSIFICATION: 435
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: US 08/008,895
6 FILING DATE: 19 JAN 1994
7 APPLICATION NUMBER: 07/909,849
8 FILING DATE: December 7, 1992
9 ATTORNEY/AGENT INFORMATION:
10 NAME: Walburg, Richard J.
11 REGISTRATION NUMBER: 42,427
12 REFERENCE TO OTHER INFORMATION:
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (213) 489 1600
15 TELEFAX: (213) 955-0440
16 TELEEX: 67 4510
17 INFORMATION FOR SEQ ID NO: 28:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 22
20 TYPE: nucleic acid
21 STRANDEDNESS: single
22 TOPOLOGY: linear
23
24 US 08 434 503 28

```

```

Query Match 0.64: Score 22: DB 1: Length 22:
Post Local Similarity 45.54: Prod. No. 1.5:
Matches 10: Conserved 1: Mismatches 0: Indels 0: Gaps 0:

```

```

DB 1 GCGCTGCTGGGATGAGTGG 22

```

```

RESULT 41
US 08 437 470 24
1 Sequence 24, Application US/08437470
2 Patent No. 5652454
3 GENERAL INFORMATION:
4 APPLICANT: Fiers, W.
5 APPLICANT: Tavernier, J.
6 TITLE OF INVENTION: TNF Mutons
7 NUMBER OF SEQUENCES: 24
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Hoffmann La Roche Inc.
10 STREET: 440 Kingsland Street
11 CITY: Nutley
12 STATE: New Jersey
13 COUNTRY: USA
14 ZIP: 07110
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: floppy disk
17 OPERATING SYSTEM: PC DOS/MS-DOS
18 SOFTWARE: Patent In Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US 08/437,470
21 FILING DATE: 20 Nov 1991
22 APPLICATION NUMBER: EP 90810901.0
23 FILING DATE: 21 Nov 1991
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Krogstad, William
26 REGISTRATION NUMBER: 44256
27 REFERENCE TO OTHER INFORMATION:
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (201) 245-4307
30 TELEFAX: (201) 245-4500
31 INFORMATION FOR SEQ ID NO: 24:

```

```

1 SEQUENCE CHARACTERISTICS:
2 LENGTH: 22 base pairs
3 TYPE: nucleic acid
4 STRANDEDNESS: single
5 TOPOLOGY: linear
6 MOLECULE TYPE: DNA (collidnucleotide)
7 FEATURE:
8 NAME/KEY: misc_feature
9 LOCATION: 1..22
10 OTHER INFORMATION:
11 OTHER INFORMATION: "probe primer"
12 OTHER INFORMATION: "probe" "probe primer used in conjunction with seq.
13 OTHER INFORMATION: ID No. 5652454, 22 & 23 to create mutons of TNF alpha
14 US-08-437-470-24

```

```

Query Match 0.64: Score 22: DB 1: Length 22:
Post Local Similarity 100.00: Prod. No. 1.5:
Matches 22: Conserved 0: Mismatches 0: Indels 0: Gaps 0:

```

```

DB 1 GCGCTGCTGGGATGAGTGG 22

```

```

RESULT 42
US 08 410 654B-46/c
1 Sequence 46, Application US/08410654B
2 Patent No. 5844976
3 GENERAL INFORMATION:
4 APPLICANT: Rene de Wael Malefyt
5 APPLICANT: De Wael Hsu
6 APPLICANT: Anne O'Garra
7 TITLE OF INVENTION: Use of Interleukin-10 to Treat
8 TITLE OF INVENTION: Septic Shock
9 NUMBER OF SEQUENCES: 61
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Schering Plough Corporation
12 STREET: 2000 Gallop Road
13 CITY: Kenilworth
14 STATE: New Jersey
15 COUNTRY: USA
16 ZIP: 07033
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: floppy disk
19 OPERATING SYSTEM: Macintosh
20 SOFTWARE: Microsoft Word 5.1a
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/410,654B
23 FILING DATE: 24-MAR-1995
24 CLASSIFICATION: 424
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/229,854
27 FILING DATE: 19-Apr-1994
28 APPLICATION NUMBER: 07/472,653
29 FILING DATE: 06-AUG-1992
30 APPLICATION NUMBER: US 07/742,129
31 FILING DATE: 06-AUG-1991
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Foulke, Cynthia L.
34 REGISTRATION NUMBER: 42,464
35 REFERENCE TO OTHER INFORMATION:
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: 908-298-2987
38 TELEFAX: 908-298-5488
39 INFORMATION FOR SEQ ID NO: 46:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 22 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: double
44 TOPOLOGY: linear

```

MOLECULE TYPE: RNA (oligonucleotide)  
US-08-410-654B-46

Query Match 0.6% Score 22 DB 2 Length 22  
Best Local Similarity 100.0% Pred No 1.5  
Matches 22 Conservative 0 Mismatches 0 Gaps 0

QY 2194 ctgagaaagagtgacacacga 2515  
|||||  
DB 22 ctgagaaagagtgacacacga 1

## RESULT 43

US-08-474-851-46/c  
Sequence 46, Application US/08474851  
Patent No. 5837232

## GENERAL INFORMATION:

APPLICANT: Rega de Madi Maletyi  
APPLICANT: Di-Hwei Hsu  
APPLICANT: Anne O'Garra  
TITLE OF INVENTION: Use of An Interleukin-10 Antagonist to Treat  
TITLE OF INVENTION: A B Cell Mediated Autoimmune Disorder  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering Plough Corporation  
STREET: 2000 Galloping Hill Road  
CITY: Kenilworth  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07033

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.5.3  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,851  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/410,654  
FILING DATE: 24-MAR-1995

APPLICATION NUMBER: US 08/229,854  
FILING DATE: 19-APR-1994  
APPLICATION NUMBER: US 07/926,853  
FILING DATE: 06-AUG-1992  
APPLICATION NUMBER: US 07/742,129  
FILING DATE: 06-AUG-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Polke, Cynthia L.  
REGISTRATION NUMBER: 32,364  
REFERENCE/WORK NUMBER: DX0221K01GD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-298-2987  
TELEFAX: 908-298-5388

INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: DNA (oligonucleotide)  
US-08-474-851-46

Query Match 0.6% Score 22 DB 2 Length 22  
Best Local Similarity 100.0% Pred No 1.5  
Matches 22 Conservative 0 Mismatches 0 Gaps 0

QY 2194 ctgagaaagagtgacacacga 2515  
|||||

DB 22 ctgagaaagagtgacacacga 1

## RESULT 44

US-08-481-566-46/c  
Sequence 46, Application US/08481566  
Patent No. 5837293

## GENERAL INFORMATION:

APPLICANT: Rega de Madi Maletyi  
APPLICANT: Di-Hwei Hsu  
APPLICANT: Anne O'Garra  
TITLE OF INVENTION: Use of Interleukin-10 to Modulate  
TITLE OF INVENTION: Inflammation of T-Cell Mediated  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation  
STREET: 2000 Galloping Hill Road  
CITY: Kenilworth  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07033

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.5.3  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,566  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/410,654  
FILING DATE: 24-MAR-1995

APPLICATION NUMBER: US 08/229,854  
FILING DATE: 19-APR-1994  
APPLICATION NUMBER: US 07/926,853  
FILING DATE: 06-AUG-1992  
APPLICATION NUMBER: US 07/742,129  
FILING DATE: 06-AUG-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Polke, Cynthia L.  
REGISTRATION NUMBER: 32,364  
REFERENCE/WORK NUMBER: DX0221K01GD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-298-2987  
TELEFAX: 908-298-5388

INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: DNA (oligonucleotide)  
US-08-481-566-46

Query Match 0.6% Score 22 DB 2 Length 22  
Best Local Similarity 100.0% Pred No 1.5  
Matches 22 Conservative 0 Mismatches 0 Gaps 0

QY 2194 ctgagaaagagtgacacacga 2515  
|||||

1 APPLICANT: Belmont, C. Frank  
 2 APPLICANT: Butler, Madeline M.  
 3 APPLICANT: Shurabon, William R.  
 4 TITLE OF INVENTION: ANTISENSE Oligonucleotide Modulation of INF- $\gamma$  Expression  
 5 FILE REFERENCE: ISPN 0422  
 6 CURRENT APPLICATION NUMBER: US/09/166,186A  
 7 CURRENT FILING DATE: 1998-10-05  
 8 NUMBER OF SEQ ID NOS: 250  
 9 SEQ ID NO 44  
 10 LENGTH: 22  
 11 TYPE: DNA  
 12 ORGANISM: Artificial Sequence  
 13 FEATURE:  
 14 OTHER INFORMATION: PCR primer  
 15 US 09 166-186 44

Query Match 0.687 Score 227 DB 41 Length 227  
 Best Local Similarity 100.00% Prod. No. 1392  
 Matches 22 Consolative 0 Mismatches 0 Indels 0 Gaps 0

QY 1602 tctctaatcagctcttgc 1623  
 DB 22 tctctaatcagctcttgc 1

Search completed: April 20, 2002, 06:44:41  
 Job Time: 11783 sec